

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2004, 02:34:49 ; Search time 4394 Seconds
(without alignments)
10623.679 Million cell updates/sec

Title: US-10-019-931-1
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 5940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO0102589.
ACCESSION AX080458
VERSION AX080458.1 GI:13159885
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
REFERENCE Varin, L. and Gidda, S.
AUTHORS Methods, compositions and genetic sequences for modulating
TITLE

flowering in plants, and plants genetically modified to flower
early and tardily

Best local Similarity 100.0%; Score 1077; DB 6; Length 1077;
Patent: WO 012589-A 1 11-JAN-2001;
Varin, Inc (CA); Gidda, Satinder (CA)

Location/Qualifiers

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ORIGIN

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Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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LOCUS Arabidopsis thaliana At5g07010 mRNA, complete cds.
DEFINITION Arabidopsis thaliana (thale cress)
ACCESSION BT008847
VERSION BT008847.1 GI:31711859
KEYWORDS FLI_CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1080)
AUTHORS Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P.,
Dale, J.M., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A.,
Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L.,
Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C.,
Wu, H.C., Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theologis, A.,
and Ecker, J.R.

TITLE

Arabidopsis ORF clones
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1080)
AUTHORS Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P.,
Dale, J.M., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A.,
Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L.,
Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C.,
Wu, H.C., Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theologis, A.,
and Ecker, J.R.

TITLE

Direct Submission
JOURNAL Submitted (13-JUN-2003) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGECC (SSP) Consortium members constructed and
sequenced the pUNI (ORF) clones using the RAFL cDNAs: Kim, C.J.,
Chen, H., Cheuk, R., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M.,
Dale, J.M., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J.,
Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L.,
Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
Yu, G., Davis, R.W., Theologis, A., and Ecker, J.R.

Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
contributed equally to this work as PIs.

FEATURES

Location/Qualifiers

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Best Local Similarity 100.0%; Pred No. 0;
Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION
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VERSION
  AY099809.1 GI:20466685
KEYWORDS
  FLI CDNA.
SOURCE
  Arabidopsis thaliana (thale cress)
  Arabidopsis thaliana
REFERENCE
  1 (bases 1 to 1347)
  Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M.,
  Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
  Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
  Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
  Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
  Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
  Direct Submission
  Submitted (24-APR-2002) DNA Sequencing and Technology Center,
  Stanford University, 855 California Avenue, Palo Alto, CA 94304,
  USA
  e-mail for correspondence: arabesequence.stanford.edu
COMMENT
  RIKEN Genomic Sciences Center (GSC) members carried out the
  collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
  Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
  Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
  Hayashizaki,Y. and Shinozaki,K.

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The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
Nguyen,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
(SSP/Stanford) contributed equally to this work as PIs.

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CDS

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RESULT 6	AY084999	LOCUS	Arabidopsis thaliana clone 1273 bp mRNA linear	PLN 14-APR-2003
DEFINITION	AY084999	VERSION	AY084999.1	GI:21403709
KEYWORDS	FLI CDNA.	SOURCE	Arabidopsis thaliana (thale cress)	
ORGANISM	Arabidopsis thaliana	REFERENCE	1 (bases 1 to 1273)	Haas, B.J., Volkovsky, N., Town, C.D., Troughan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O., and Salzberg, S.L.
AUTHORS	Full-length messenger RNA sequences greatly improve genome annotation	TITLE	Genome Biol. 3 (6), RESEARCH0029 (2002)	
JOURNAL	22088475	MEDLINE	12093376	
PUBMED	2	AUTHORS	2 (bases 1 to 1273)	Brover, V., Troughan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
TITLE	Full-length cDNA from Arabidopsis thaliana	JOURNAL	Unpublished	
REFERENCE	3 (bases 1 to 1273)	AUTHORS	Brover, V., Troughan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.	
TITLE	Direct Submission	JOURNAL	Submitted (11-MAR-2002)	Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
COMMENT	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.			
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ORIGIN

Query Match 80.1%; Score 863; DB 8; Length 1236;
Best Local Similarity 89.9%; Pred. No. 2.2e-256;
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ACCESSION AX080460
VERSION AX080460.1 GI:13159886
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Varin,L. and Gidda,S.
METHODS Compositions and genetic sequences for modulating
flowering in plants, and plants genetically modified to flower
early and tardily
Patent: WO 0102589-A 3 11-JAN-2001;
Varin, Luc (CA); Gidda, Satinder (CA)
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Best Local Similarity 89.8%; Pred. No. 2.3e-250;
Matches 945; Conservative 0; Mismatches 89; Indels 18; Gaps 3;
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VERSION	BT006241.1		
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SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
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AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1044)		
	Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P., Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Heuan, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.		
TITLE	Arabidopsis ORF clones		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1044)		
AUTHORS	Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P., Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Heuan, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.		

TITLE	JOURNAL	COMMENT	FEATURES	source	CDS	ORIGIN	Query Match	78.3%	Score	843.6;	DB	8;	Length	1044;
							Best Local Similarity	89.8%	Pred. NO.	2.3e-250;				
							Matches	945;	Conservative	0;	Mismatches	89;	Indels	18;
							Gaps	3;						
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QY	151	GATTCCTCTCTTAAGAGAGAGGATGAGAACTCGTTACCTTTTACCTATTCCTCAAGGGTTT	210											
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Ecker, J.R.
 Direct Submission
 Submitted (17-APR-2003) Salk Institute Genomic Analysis Laboratory
 (StGnal), Plant Biology Laboratory, The Salk Institute for
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
 USA
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL CDNA: 'RIKEN
 Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
 Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members constructed and
 sequenced the PUNI (ORF) clones using the RAFL cDNAs: Kim, C.J.,
 Chen, H., Cheuk, R., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M.,
 Dale, J.M., Heuan, V.W., Jones, T., Karlin-Neumann, G., Lam, B.,
 Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J.,
 Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,
 Yamada, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A., and
 Ecker, J.R.

Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
 this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
 contributed equally to this work as PIs.

Location/Qualifiers

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Qy 448 AACGAGATGTCCTCGATCTCTCGGTCGAGTCCAAAGAACTTTCGAAACCTTCA 507
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RESULT 10
AC135566
LOCUS
DEFINITION
AC135566
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

AC135566
Medicago truncatula clone mth2-22g8, WORKING DRAFT SEQUENCE, 3 ordered pieces.
AC135566
HTG; HTGS PHASE2; HTGS DRAFT.
Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
1 (bases 1 to 111989)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-22g8
Unpublished
2 (bases 1 to 111989)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,

Qy 109 GAAGAAGTGAAGGCTAAGCTGCGAGTTCAGAGATGTTGGATTCTCTTCCTTAAGGAG 168
Db 43192 GAAGAACAAGTCAACTTAGCCAGAAACAAAGAACTAATCTCTTCTCTTCCAGAGAG 43251
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Qy 289 GCCACCATACCTTAATCCGTTACACCTGCTTAAAGCTTTAACTTCCACCATCCTTAAC 348
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ORIGIN

Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (18-OCT-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 111989)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (12-DEC-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Dec 12, 2003 this sequence version replaced gi:39573775.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 11239: contig of 11239 bp in length
* 11240 11339: gap of unknown length
* 11340 20610: contig of 9271 bp in length
* 20611 20710: gap of unknown length
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location/Qualifiers
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DEFINITION
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Medicago truncatula clone mth2-10020, WORKING DRAFT SEQUENCE, 2
unpublished pieces.
AC146342
VERSION
AC146342.4 GI:38488819
HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
Medicago truncatula
SOURCE
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 113531)
Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.
and Roe, B.A.
Medicago truncatula BAC clone mth2-10020
Unpublished
REFERENCE
2 (bases 1 to 113531)
Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.
and Roe, B.A.
Direct Submission
Submitted (12-AUG-2003) Department of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE
3 (bases 1 to 113531)
Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.
and Roe, B.A.
Direct Submission
Submitted (21-NOV-2003) Department of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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OK 73019, USA
On Nov 21, 2003 this sequence version replaced gi:38371842.
----- Genome Center
Center: Department of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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QY 780 AGACACATCGAGACCAACTTGAAGAGCTTGCACCTTTCTTAGAGTCTCTTTTCACCGA 839
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QY 840 AGAGAGAGAACGAAAGGAGTGTGAAGGCTATCCCGAGCTGTGTAGCTTCGAGAAATCT 899
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QY 960 GTTTCGAAAGGAGAGTGAATGGGTAACTATTGTGACCTTCACAAAGTGGAAAG 1019
Db 108393 CTTTCGAAAGGAGAAATAGAGATTGGTAAATTAATCTTTCTCTTCATGATAGAAAG 108334
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RESULT 12
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DEFINITION Medicago truncatula clone mth2-7k13, complete sequence.
ACCESSION AC144726
VERSION AC144726.6 GI:34365847
KEYWORDS HTG.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 138586)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Medicago truncatula BAC Clone mth2-7k13
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 138586)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 3 (bases 1 to 138586)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 4 (bases 1 to 138586)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT On Aug 30, 2003 this sequence version replaced gi:32567849.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
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FEATURES
Location/Qualifiers

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source

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/clone="mth2-7k13"
/clone_lib="Medicago truncatula BAC library H2"

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Matches 540; Conservative 0; Mismatches 424; Indels 9; Gaps 2;

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Db 33012 TACATTGTGTAGTTTGTAGAGCTTAGCACTTGGAGATCAATAGAAACGGGAAATTT 32953
QY 935 TCAAGAACTTTGAGAAATCGATTCTTTTTCGAAAGGAGAGTGAAGTCAITGGGTTAACT 994
Db 32952 CGTCGAAATTTGAAAAACAAGAACTTTTTCGCTCTTGGCAAAAGTTGGAGATTGAAAAATC 32893
QY 995 ATTTGTCACTTTCACAGTGGAAAGATTGTACGCTTAGTGGATGACAAAGTTAGTGGAT 1054

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QY 1060 CTCACCTTCAGGTGAGC 1077
Db 21846 CTATCAATTAAAGGGTGC 21829

RESULT 14
AC144476
LOCUS
DEFINITION
Medicago truncatula clone mth2-10a6, WORKING DRAFT SEQUENCE, 3
ordered pieces.
ACCESSION
AC144476
VERSION
GI:34576471
KEYWORDS
HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE
Medicago truncatula
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 119317)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-10a6
Unpublished
2 (bases 1 to 119317)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (22-APR-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 119317)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (12-SEP-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Sep 11, 2003 this sequence version replaced gi:34365846.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 101223: contig of 101223 bp in length
* 101224 101323: gap of unknown length
* 101324 108389: contig of 7066 bp in length
* 108390 108499: gap of unknown length
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Best Local Similarity 58.4%; Pred. No. 2,1e-66;
Matches 529; Conservative 0; Mismatches 352; Indels 25; Gaps 4;
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QY 467 TCTCGGGTCTAGCCAGTCCCAAGACGTTTCGCAACCACTTACCGTTCCGTTCCCTTAAAGG 526
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RESULT 15
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unordered pieces.
ACCESSION
AC147431
VERSION
GI:39652661
KEYWORDS
HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE
Medicago truncatula (barrel medic)

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ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE 1 (bases 1 to 147510)
AUTHORS Qin, B., Lin, S. and Roe, B. A.
TITLE Medicago truncatula BAC Clone mth2-88g17
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 147510)
AUTHORS Qin, B., Lin, S. and Roe, B. A.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Department of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

REFERENCE 3 (bases 1 to 147510)
AUTHORS Qin, B., Lin, S. and Roe, B. A.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2003) Department of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

COMMENT On Dec 10, 2003 this sequence version replaced gi:38708072.
----- Genome Center
Center: Department of Chemistry and Biochemistry
The University of Oklahoma
Center code: UONOR

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 3309: contig of 3309 bp in length
* 3310 3409: gap of unknown length
* 3410 5938: contig of 2529 bp in length
* 5939 6039: gap of unknown length
* 6039 13001: contig of 6963 bp in length
* 13002 13101: gap of unknown length
* 13102 22529: contig of 9428 bp in length
* 22530 22630: gap of unknown length
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ORIGIN

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Best Local Similarity 58.4%; Mismatches 352; Indels 25; Gaps 4;
Matches 529; Conservative 0;
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DB 125147 AACCAATTATTTTATTTTTCCTCAAGGTTTGGGCTCCACCATCTCCAAATAAATCTAT 125206
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DB 125327 TCTCTCTTTTAG-----AGAATCATCAATTACTTATCATCTAATCTCATGAACCTG 125377
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
9318.349 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	229.2	21.3	981	7	Abz42036 Arabidops
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ALIGNMENTS

RESULT 1

AAF29177
ID AAF29177 standard; DNA; 1077 BP.

XX AAF29177;

DT 09-APR-2001 (first entry)

DE Hydroxyjasmonic acid sulfotransferase AtST2a gene.

KW Hydroxyjasmonic acid sulfotransferase; AtST2a; flowering time; cabbage;
KW jasmonate; genetically modified plant; lettuce; sugar cane; carrot;
KW increase vegetative growth; biomass increase; ds.

OS Arabidopsis thaliana.

XX WO200102589-A2.

XX 11-JAN-2001.

PF 06-JUL-2000; 2000WO-CA000801.

PR 06-JUL-1999; 99CA-02274873.

XX (VARI/) VARIN L.

PA (GIDD/) GIDDA S.

PI Varin L, Gidda S;

DR WPI; 2001-159272/16.

XX P-PSDB; AAB49722.

XX Methods for modulating flowering in plants, particularly useful for
PT plants used in the food-processing industry, involves modifying the
PT endogenous level of compounds of the jasmonate family.

PS Claim 38; Fig 7; 50pp; English.

XX This invention relates to a method for modulating flowering in a plant.
CC The method comprises modifying the endogenous level of at least one
CC compound of the jasmonate family in a plant. The methods are used to
CC produce plants which are genetically modified to flower early or tardily
CC when compared to a corresponding plant that is not genetically modified,
CC where the modified plant has an increased (flower early) or lowered
CC (flower tardily) level of jasmonic acid, or a compound of the jasmonate
CC family. The method is useful for modulating flowering, particularly for

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Db	124	AAGCTCAGCTCCTTAAGAGAGCAAACTCGGAGCTCCGAAAGCCGAAAGATGAA	183
Qy	121	GGGTAAGCTCGAGTTCCAGAGATGTTGGATTCTTCTTAAGAGAGAGATCGAGA	180
Db	184	GGGTAAGCTCGAGTTCCAGAGATGTTGGATTCTTCTTAAGAGAGAGATCGAGA	243
Qy	181	ACTCGTTACCTTACCTATTCCAGGGTTTGGTCCCAAGCCAAAGAGATTCAGGCATC	240
Db	244	ACTCGTTACCTTACCTATTCCAGGGTTTGGTCCCAAGCCAAAGAGATTCAGGCATC	303
Qy	241	ATGTCCTTCCAAAACATTTCCAACTCCCTCGAAAACGACGTCGTTCTCGCCACCATACCT	300
Db	304	ATGTCCTTCCAAAACATTTCCAACTCCCTCGAAAACGACGTCGTTCTCGCCACCATACCT	363
Qy	301	AAATCCGGTACAACTCGGCTAAAGCTTTTAACTTTTACCATCTCTTAACCGTCAACCGTTT	360
Db	364	AAATCCGGTACAACTCGGCTAAAGCTTTTAACTTTTACCATCTCTTAACCGTCAACCGTTT	423
Qy	361	GATCCGGTTGCTCGAGTACCAACACCTCTTTTCACTTCCAAACCTCATGACCTTGTA	420
Db	424	GATCCGGTTGCTCGAGTACCAACACCTCTTTTCACTTCCAAACCTCATGACCTTGTA	483
Qy	421	CTTTCTTCGAGTCAAGCTTTACGCCAAGAGATGTTCCGATCTCTCGGTCTAGCC	480
Db	484	CTTTCTTCGAGTCAAGCTTTACGCCAAGAGATGTTCCGATCTCTCGGTCTAGCC	543
Qy	481	AGTCCAGAAAGCTTCCGAAACCACTTACCGTTCGGTTCCTTAAGGAAACGATCGAGAAA	540
Db	544	AGTCCAGAAAGCTTCCGAAACCACTTACCGTTCGGTTCCTTAAGGAAACGATCGAGAAA	603
Qy	541	CCCGTGTGAAGGTCGTGTACTTGTGCGGAAACCGTTTGACACATTCATCTCTTGTGG	600
Db	604	CCCGTGTGAAGGTCGTGTACTTGTGCGGAAACCGTTTGACACATTCATCTCTTGTGG	663
Qy	601	CATTACCAACACATCAATCCGAGTCAGTACCCAGCTCTGTAGACCAAGCTTTT	660
Db	664	CATTACCAACACATCAATCCGAGTCAGTACCCAGCTCTGTAGACCAAGCTTTT	723
Qy	661	GATCTGTATTCGGGGAGTGTATCGGGTTTGGCCCGTTTGGGAAACATGTTGGGATAC	720
Db	724	GATCTGTATTCGGGGAGTGTATCGGGTTTGGCCCGTTTGGGAAACATGTTGGGATAC	783
Qy	721	TGGAGAGAGCTTGAAGAGACCAAGAGAACTCTTTTAAAGTACGAGGATCTCAAA	780
Db	784	TGGAGAGAGCTTGAAGAGACCAAGAGAACTCTTTTAAAGTACGAGGATCTCAAA	843
Qy	781	GACGACATCGAGACCACTTGAAGAGGCTTCCAACTTTCTTAGAGCTTCTTCCACCGAA	840
Db	844	GACGACATCGAGACCACTTGAAGAGGCTTCCAACTTTCTTAGAGCTTCTTCCACCGAA	903
Qy	841	GAAGAGGAAAGGAGTGTGAAGGCTATCGCCGAGCTGTGTAGCTTCGAGAACTGTG	900
Db	904	GAAGAGGAAAGGAGTGTGAAGGCTATCGCCGAGCTGTGTAGCTTCGAGAACTGTG	963
Qy	901	AAGAAGTTGGAGGTGAACAGCTCAACCAAGTCGATCAGAACCTTTGAGAACTCTTG	960
Db	964	AAGAAGTTGGAGGTGAACAGCTCAACCAAGTCGATCAGAACCTTTGAGAACTCTTG	1023
Qy	961	TTTCCGAAGGAGAGTGAAGTGAAGTGGTTAACTATTTGTACCTTCAAGTGGAAAGA	1020
Db	1024	TTTCCGAAGGAGAGTGAAGTGAAGTGGTTAACTATTTGTACCTTCAAGTGGAAAGA	1083
Qy	1021	TTGTGAGCTTGTGATGACAGTGTAGTGTGATCTGGTCTCACTTCAGGTTGAGC	1077
Db	1084	TTGTGAGCTTGTGATGACAGTGTAGTGTGATCTGGTCTCACTTCAGGTTGAGC	1140

RESULT 3
AAC47848
ID AAC47848 standard; DNA; 1273 BP.
XX
AAC47848;
XX
18-OCT-2000 (first entry)
XX
Arabidopsis thaliana DNA fragment SEQ ID NO: 55342.
XX
Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
EP1033405-A2.
XX
06-SEP-2000.
XX
25-FEB-2000; 2000EP-00301439.
XX
25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130499P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999;	99US-0139457P.	PR 20-AUG-1999;	99US-0149722P.
PR 18-JUN-1999;	99US-0139458P.	PR 20-AUG-1999;	99US-0149723P.
PR 18-JUN-1999;	99US-0139459P.	PR 20-AUG-1999;	99US-0149923P.
PR 18-JUN-1999;	99US-0139460P.	PR 23-AUG-1999;	99US-0149902P.
PR 18-JUN-1999;	99US-0139461P.	PR 23-AUG-1999;	99US-0149930P.
PR 18-JUN-1999;	99US-0139462P.	PR 25-AUG-1999;	99US-0150566P.
PR 18-JUN-1999;	99US-0139463P.	PR 26-AUG-1999;	99US-0150884P.
PR 18-JUN-1999;	99US-0139750P.	PR 27-AUG-1999;	99US-0151065P.
PR 21-JUN-1999;	99US-0139763P.	PR 27-AUG-1999;	99US-0151066P.
PR 21-JUN-1999;	99US-0139817P.	PR 27-AUG-1999;	99US-0151080P.
PR 22-JUN-1999;	99US-0139899P.	PR 30-AUG-1999;	99US-0151303P.
PR 23-JUN-1999;	99US-0140353P.	PR 31-AUG-1999;	99US-0151438P.
PR 23-JUN-1999;	99US-0140354P.	PR 01-SEP-1999;	99US-0151930P.
PR 24-JUN-1999;	99US-0140695P.	PR 07-SEP-1999;	99US-0152363P.
PR 28-JUN-1999;	99US-0140823P.	PR 10-SEP-1999;	99US-0153070P.
PR 29-JUN-1999;	99US-0140931P.	PR 13-SEP-1999;	99US-0153758P.
PR 30-JUN-1999;	99US-0141287P.	PR 13-SEP-1999;	99US-0154018P.
PR 01-JUL-1999;	99US-0141842P.	PR 16-SEP-1999;	99US-0154039P.
PR 01-JUL-1999;	99US-0142154P.	PR 20-SEP-1999;	99US-0154779P.
PR 02-JUL-1999;	99US-0142055P.	PR 22-SEP-1999;	99US-0155139P.
PR 06-JUL-1999;	99US-0142390P.	PR 23-SEP-1999;	99US-0155486P.
PR 08-JUL-1999;	99US-0142803P.	PR 24-SEP-1999;	99US-0155659P.
PR 09-JUL-1999;	99US-0142920P.	PR 28-SEP-1999;	99US-0156458P.
PR 12-JUL-1999;	99US-0142977P.	PR 29-SEP-1999;	99US-0156596P.
PR 13-JUL-1999;	99US-0143542P.	PR 04-OCT-1999;	99US-0157117P.
PR 14-JUL-1999;	99US-0143624P.	PR 05-OCT-1999;	99US-0157533P.
PR 15-JUL-1999;	99US-0144005P.	PR 06-OCT-1999;	99US-0157865P.
PR 16-JUL-1999;	99US-0144085P.	PR 07-OCT-1999;	99US-0158029P.
PR 16-JUL-1999;	99US-0144086P.	PR 08-OCT-1999;	99US-0158232P.
PR 19-JUL-1999;	99US-0144325P.	PR 12-OCT-1999;	99US-0158369P.
PR 19-JUL-1999;	99US-0144331P.	PR 13-OCT-1999;	99US-0159293P.
PR 19-JUL-1999;	99US-0144332P.	PR 13-OCT-1999;	99US-0159294P.
PR 19-JUL-1999;	99US-0144333P.	PR 14-OCT-1999;	99US-0159295P.
PR 19-JUL-1999;	99US-0144334P.	PR 14-OCT-1999;	99US-0159329P.
PR 20-JUL-1999;	99US-0144352P.	PR 14-OCT-1999;	99US-0159331P.
PR 20-JUL-1999;	99US-0144352P.	PR 14-OCT-1999;	99US-0159637P.
PR 20-JUL-1999;	99US-0144362P.	PR 14-OCT-1999;	99US-0159638P.
PR 21-JUL-1999;	99US-0144884P.	PR 18-OCT-1999;	99US-0159584P.
PR 21-JUL-1999;	99US-0145086P.	PR 21-OCT-1999;	99US-0160741P.
PR 21-JUL-1999;	99US-0145088P.	PR 21-OCT-1999;	99US-0160767P.
PR 22-JUL-1999;	99US-0145085P.	PR 21-OCT-1999;	99US-0160768P.
PR 22-JUL-1999;	99US-0145087P.	PR 21-OCT-1999;	99US-0160770P.
PR 22-JUL-1999;	99US-0145089P.	PR 21-OCT-1999;	99US-0160814P.
PR 22-JUL-1999;	99US-0145192P.	PR 21-OCT-1999;	99US-0160815P.
PR 23-JUL-1999;	99US-0145145P.	PR 22-OCT-1999;	99US-0160800P.
PR 23-JUL-1999;	99US-0145218P.	PR 22-OCT-1999;	99US-0160981P.
PR 23-JUL-1999;	99US-0145224P.	PR 22-OCT-1999;	99US-0160989P.
PR 26-JUL-1999;	99US-0145276P.	PR 25-OCT-1999;	99US-0161404P.
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PR 27-JUL-1999;	99US-0145918P.	PR 25-OCT-1999;	99US-0161406P.
PR 27-JUL-1999;	99US-0145919P.	PR 26-OCT-1999;	99US-0161359P.
PR 28-JUL-1999;	99US-0145951P.	PR 26-OCT-1999;	99US-0161360P.
PR 02-AUG-1999;	99US-0146386P.	PR 26-OCT-1999;	99US-0161361P.
PR 02-AUG-1999;	99US-0146388P.	PR 28-OCT-1999;	99US-0161920P.
PR 02-AUG-1999;	99US-0146389P.	PR 28-OCT-1999;	99US-0161922P.
PR 03-AUG-1999;	99US-0147038P.	PR 28-OCT-1999;	99US-0161993P.
PR 04-AUG-1999;	99US-0147204P.	PR 29-OCT-1999;	99US-0162142P.
PR 04-AUG-1999;	99US-0147302P.		
PR 05-AUG-1999;	99US-0147192P.		
PR 05-AUG-1999;	99US-0147260P.		
PR 06-AUG-1999;	99US-0147303P.		
PR 06-AUG-1999;	99US-0147416P.		
PR 09-AUG-1999;	99US-0147493P.		
PR 09-AUG-1999;	99US-0147935P.		
PR 10-AUG-1999;	99US-0148171P.		
PR 11-AUG-1999;	99US-0148319P.		
PR 12-AUG-1999;	99US-0148341P.		
PR 13-AUG-1999;	99US-0148565P.		
PR 13-AUG-1999;	99US-0148684P.		
PR 16-AUG-1999;	99US-0149368P.		
PR 17-AUG-1999;	99US-0149175P.		
PR 18-AUG-1999;	99US-0149426P.		

Query Match 99.7%; Score 1073.8; DB 3; Length 1273;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1075; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATGGCTACCTCAAGCATGAAGAGCATTCCAATGGGATCCCAAGTTCTCCATGTGTAC	60
DB	66	ATGGCGACCTCAAGCATGAAGAGCATTCCAATGGGATCCCAAGTTCTCCATGTGTAC	125
QY	61	AAGCTCGAGCTCCTTAAAGAGGCAAACTCCGACGTCCTCGAAGCCGGAAGAGATGAA	120
DB	126	AAGCTCGAGCTCCTTAAAGAGGCAAACTCCGACGTCCTCGAAGCCGGAAGAGATGAA	185
QY	121	GGCTAAGCTCGGATTCCAAGAGATGTGATTCCTCTTAAGAGAGAGATGAGA	180

Db 186 GGGCTAAGTCGAGTTCCAGAGATGTTGGATTCTCTTCTTAAGAGAGAGATGGAGA 245
Qy 181 ACTCGTTACCTTTACCTATTCCAGGGTTTGGTCCAGCCAAAGAGATTCAAGCCATC 240
Db 246 ACTCGTTACCTTTACCTATTCCAGGGTTTGGTCCAGCCAAAGAGATTCAAGCCATC 305
Qy 241 ATGTCTTTTCAAAAACATTTCCAAATCCCTCGAAAAACGACGTCTCTTCGCCACCATACCT 300
Db 306 ATGTCTTTTCAAAAACATTTCCAAATCCCTCGAAAAACGACGTCTCTTCGCCACCATACCT 365
Qy 301 AAATCCGGTACACCTGGCTAAAGCTTTAACTTTACCGATCTTAAACCGTCAACCGTTT 360
Db 366 AAATCCGGTACACCTGGCTAAAGCTTTAACTTTACCGATCTTAAACCGTCAACCGTTT 425
Qy 361 GATCCGGTTGCTCGAGTACCAACCCCTCTTTTCACTTCCAAACCTCATGACCTTGTGA 420
Db 426 GATCCGGTTGCTCGAGTACCAACCCCTCTTTTCACTTCCAAACCTCATGACCTTGTGA 485
Qy 421 CCTTTCTCGAGTACAAAGCTTTACGCAACGAGATGTTCCCGATCTCTCGGTCTAGCC 480
Db 486 CCTTTCTCGAGTACAAAGCTTTACGCAACGAGATGTTCCCGATCTCTCGGTCTAGCC 545
Qy 481 AGTCCAGAGAGTTCCGCAACCATCTTACGTTCCGTTCCCTAAAGGAAACGATCGAGAAA 540
Db 546 AGTCCAGAGAGTTCCGCAACCATCTTACGTTCCGTTCCCTAAAGGAAACGATCGAGAAA 605
Qy 541 CCCGGTGTGAAGTGTGTACTTTGTGCGGAACCCGTTTGACACATTCATCTCTTCGTGG 600
Db 606 CCCGGTGTGAAGTGTGTACTTTGTGCGGAACCCGTTTGACACATTCATCTCTTCGTGG 665
Qy 601 CATTAACCAACACATCAAAATCCGATCAGTACGACCCATCTTCTAGACCAAGCTTTT 660
Db 666 CATTAACCAACACATCAAAATCCGATCAGTACGACCCATCTTCTAGACCAAGCTTTT 725
Qy 661 GATCTGTATTGCGGGAGTGTATCGGGTTTGGCCGTTTGGGAAACACATGTTGGGATAC 720
Db 726 GATCTGTATTGCGGGAGTGTATCGGGTTTGGCCGTTTGGGAAACACATGTTGGGATAC 785
Qy 721 TGGAGAGAGAGCTTGAAGAGACCAAGAAAGTCTTTTAAAGGTACGAGGATCTCAAA 780
Db 786 TGGAGAGAGAGCTTGAAGAGACCAAGAAAGTCTTTTAAAGGTACGAGGATCTCAAA 845
Qy 781 GACCACATCGAGACCAACTTGAAGAGCTTGCACATTTCTTAGAGCTTCCCTTTCCCGAA 840
Db 846 GACCACATCGAGACCAACTTGAAGAGCTTGCACATTTCTTAGAGCTTCCCTTTCCCGAA 905
Qy 841 GAAGAGAAACGAAAGGAGTTGTGAAGGCTATCGCGAGCTGTGTAGTTCGAGATCTG 900
Db 906 GAAGAGAAACGAAAGGAGTTGTGAAGGCTATCGCGAGCTGTGTAGTTCGAGATCTG 965
Qy 901 AAGAGTTGAGGTTGAACAGTCAAAACAGTCCGATCAAGAACTTTGAGATCGATCTTGG 960
Db 966 AAGAGTTGAGGTTGAACAGTCAAAACAGTCCGATCAAGAACTTTGAGATCGATCTTGG 1025
Qy 961 TTTCCGAAAGAGAGAGTGAAGTGTGAGTTAACTATTGTCACTTCAAAAGTGAAGA 1020
Db 1026 TTTCCGAAAGAGAGAGTGAAGTGTGAGTTAACTATTGTCACTTCAAAAGTGAAGA 1085
Qy 1021 TTGTCAGCTTAGTGATGACAGAGTTAGGTGGATCTGGTCTCACTTCAGTTGAGC 1077
Db 1086 TTGTCAGCTTAGTGATGACAGAGTTAGGTGGATCTGGTCTCACTTCAGTTGAGC 1142

RESULT 4

AAF29178 standard; DNA; 1041 BP.
XX
AC AAF29178;
XX
DT 09-APR-2001 (first entry)
XX
DE Hydroxyjasmonic acid sulfoltransferase AtSt2b gene.
XX

KW Hydroxyjasmonic acid sulfoltransferase; AtSt2b; flowering time; cabbage;
KW jasmonate; genetically modified plant; lettuce; sugar cane; carrot;
XX increase vegetative growth; biomass increase; ds.
OS Arabidopsis thaliana.

XX WO200102589-A2.

XX 11-JAN-2001.

XX 06-JUL-2000; 2000WO-CA000801.

XX 06-JUL-1999; 99CA-02274873.

XX (VARI/) VARIN L.

XX (GIDD/) GIDDA S.

XX Varin L, Gidda S;

XX WPI; 2001-159272/16.

XX P-PSDB; AAB49723.

XX Methods for modulating flowering in plants, particularly useful for
plants used in the food-processing industry, involves modifying the
endogenous level of compounds of the jasmonate family.

XX Claim 38; Fig 9; 50pp; English.

XX This invention relates to a method for modulating flowering in a plant.
The method comprises modifying the endogenous level of at least one
compound of the jasmonate family in a plant. The methods are used to
produce plants which are genetically modified to flower early or tardily
when compared to a corresponding plant that is not genetically modified,
where the modified plant has an increased (flower early) or lowered
(flower tardily) level of jasmonic acid, or a compound of the jasmonate
family. The method is useful for modulating flowering, particularly for
plants that are used in the food-processing industry and plants with
horticultural value. The method is particularly useful for e.g. delaying
flowering time in crops like lettuce, cabbage, sugar cane or carrots,
which results in increased vegetative growth and biomass. The present
sequence represents the Arabidopsis thaliana AtSt2b gene, which encodes
an hydroxyjasmonic acid sulfoltransferase protein, which can be used in
the method of the invention

XX Sequence 1041 BP; 287 A; 241 C; 242 G; 271 T; 0 U; 0 Other;

Query Match 78.3%; Score 843.6; DB 4; Length 1041;

Best Local Similarity 89.8%; Pred. No. 1.8e-258;

Matches 945; Conservative 0; Mismatches 89; Indels 18; Gaps 3;

Qy 31 ATGGCGATCCCAAGTTTCTCCATGTGTCAAGCTCCAGAGCTCCCTTAAAGAGGCAAACT 90

Db 1 ATGGCGATCCCAAGTTTCTCCATGTGTCAAGCTCCAGAGCTCCCTTAAAGAGGCAAAAGC 60

Qy 91 CGCGACGTCCCGAAGCCGAAAGAGATGAAGGGCTAAGCTCGAGTTCGAAGATGTG 150

Db 61 G-----AAGGCCAAGAAAGAGAGGGCTAAGCTACGAGTTCGAAGATGTG 108

Qy 151 GATTCCTCTTCTTAGGAGAGAGGATGGAGAACTCGTTACCTTTACCTTATTCGAAGGGTTT 210

Db 109 GACTCTCTTCTTAGGAGAGAGGAGCGGAGAAATGTTACCTTTACTTATTCGAAGGGTTT 168

Qy 211 TGGTGCCCAAGCCAAAGAGATTCAAGCCATCATGTCTTTTCCAAAAACATTTCCAATCCCTC 270

Db 169 CGGTGCCAAGCTAAGGAGATTCAAGCTATACGCTTTTCCAAAAACATTTTCAGTCCCTT 228

Qy 271 GMAAACGAGCTGTTCTCGCCACCATACCTAAATCCGCTACCACTGCTGCTAAAGCTTTA 330

Db 229 CCAGACGAGCTGTGCTCGCCACCATACCTAAATCTGCGCAACCTGTTTAAAGCTTTA 288

Qy 331 ACTTTTCAACATCTTAAACCGTCAACCGGTTTGTATCCGGTTGCC---TCGAGTACCAACAC 387

Db 289 ACTTTTCAACATCTTAAACCGTCAACCGGTTTGTATCCGGTTTCTCATCAAGTTCGAGCAC 348

772 GATCTCAAGACGACATCGAGACCAACTTGAAGAGGCTTGCAACTTCTTCTAGAGCTTCCT 831
 688 GAGCTTAAGACGACGACGAGTTGAGATGAAGCGGATCGCGAGTCTTGGAAATGTGC 747
 832 TTCACCGAAGAGGAGGAGGAGTGTGAAGCTATCCCGAGCTGTGAGCTTC 891
 748 TTTATTGAAGAGGAGAA-----GTGAGAGAGATTGGAAGTTGTGAGCTTT 795
 892 GAGAACTCTGAAGAGTTGGAGGTGAACAAGTCAACCAAGTCGATCAAGAACTTTGAGAAT 951
 796 GAGAGTTTAACTAATTGGAAGTTTAAACAAGAGGGAATTCGCAATGGAATAGAGACT 855
 952 CGATCTCTGTTCCGAAGGAGAGTGAAGTGGTGAAGTGAAGTGAAGTGAAGTGAAGT 1011
 856 AAAAATCTTCTTTAGAAAAGGAGGATTTGGAGGATGGAGAGATACTTTGAGTGAATG 915
 1012 GTGGAAGAGATTGTGAGCTTGTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1067
 916 GCAGAGGAAATTGATAGAACCAATTGAAGAGAGTTTAAAGGTTCTGGTCTTAATT 971

RESULT 6
 ID ABZ14244 standard; DNA; 981 BP.

AC ABZ14244;

XX 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2049.

XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX Arabidopsis thaliana.

XX WO200216655-A2.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US026885.

XX 24-AUG-2000; 2000US-0227866P.

XX 26-JAN-2001; 2001US-0264647P.

XX 22-JUN-2001; 2001US-0300111P.

XX (SCRI) SCRIPPS RES INST.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

XX Identifying a stress condition to which a plant cell has been exposed and

XX producing plants with increased tolerance to these abiotic stresses.

XX Claim 144; SEQ ID NO 2049; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant
 XX cell has been exposed, comprising: (a) contacting nucleic acid
 XX representative of expressed polynucleotides in the plant cell with an
 XX array or probes representative of the plant cell genome; and (b)
 XX detecting a profile of expressed polynucleotides in the plant cell
 XX characteristic of a stress response. The method is useful in the
 XX production of transgenic plants, cells and seeds and in producing plants
 XX with increased tolerance to abiotic stress. The present sequence is that
 XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 XX in methods of the invention. Note: The sequence data for this patent is
 XX not represented in the printed specification but is based on sequence
 XX information supplied to Derwent by the European Patent Office

XX Sequence 981 BP; 283 A; 178 C; 228 G; 292 T; 0 U; 0 Other;

Query Match 21.3%; Score 229.2; DB 6; Length 981;
 Best Local Similarity 54.9%; Pred. No. 3.8e-62;
 Matches 525; Conservative 0; Mismatches 413; Indels 18; Gaps 3;
 QY 112 GAAGATGAAGGGCTAAGCTGCGAGTTCCAAGAGATGTTGGATTTCTTCTTAAAGAGAGA 171
 DB 34 GAGATGAGATCTGACACAGAAAGAGCTCTGATCTCTCTCTCTTAAAGAGAA 93
 QY 172 GATGAGAGATCTGCTTACCTTCTTCAAGGGTTTGGTGCACAGCAAGAGATT 231
 DB 94 GGTGTTGTTAGTGAAGTATATGATTTCAAGGACTTTGGCACAACAAGCTATT 153
 QY 232 CAAGCCATCATGCTTTCCAAAAACATTTCCAAATCCCTCGAAAAAGAGCTGTTCTCGCC 291
 DB 154 CAAGAACTTGAATCTGCAAAAACGCTTTGAAGTAAAGATTCCGACATTTATCTGTC 213
 QY 292 ACCATPACCTAAATCCGTTACAACTGGCTAAAAGCTTTTAACTTTACCATCTTAAACGCT 351
 DB 214 ACTAATCTAAATCAGTACCACTTGGTTAAAGCTCTTGTCTTCTCTCTCTTAAACGA 273
 QY 352 CACCGGTTGATCCGTTGCTCGAGTACCAACCACTCTTTTCACTTCCAAACCTCAT 411
 DB 274 CACAAGTT---TCCAGTTTCTTCTTCTGTAACCATCTCTTCTGTCACCAATCCACAC 330
 QY 412 GACCTTGTACCTTCTTCTGAGTACAAAGCTTTACGCAACGAGATGTTCCGAGTCTCTCG 471
 DB 331 CTTCTTGTGCTTCTTCTGNAAGGATTTTACGAGTCCCGAGATT---CGATTTCTCC 387
 QY 472 GGTCTAGCCAGTCCAAAGACGTTGCAACCACTTACCGTTCCGTTCCCTTAAAGAAACG 531
 DB 388 AGTTTGCCTTCTTCCAAGACTGATGAACACGACATATGCAATCTTTCGCTCCCGAGTCT 447
 QY 532 ATCGAGAAACCGGTGTAAGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 591
 DB 448 GTTAAGAGCTGCTTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTA 507
 QY 592 TCTTCGTGGCTATACCAACAACATCAATCCAGTCACTGAGCCAGCTTCTTCTTCTTCTTCT 651
 DB 508 TCTTTATGGCATTTTGGGAAAAAGCTAGCTCTCTGAGGAAACCGCGGATTTATCTTATCGAA 567
 QY 652 CAAGCTTTTGTATCTGTTTGGGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 711
 DB 568 AAAGCGTTGAGCGTTTGTGTAAGGAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGT 627
 QY 712 TTGGGATATCTGGAGAGAGAGCTTGAAGAGACCAAGAGAAAGTCTTCTTCTTCTTCTTCT 771
 DB 628 TTGGAGTACTGTTATGCAAGCGCGAGAAATCCGAACAAGTCTTGTGTTGTTACTTACGAG 687
 QY 772 GATCTCAAGAGCAGATCGAGACCACTTGAAGAGGCTTGAAGTGTGCTTCTTCTTCTTCTTCT 831
 DB 688 GAGCTTAAAGAGCAGACCGAAGTTGAGATGAAGCGGATTCGCGGAGTTCTTGGAAATGTGGC 747
 QY 832 TTCACCGAAGAGAGGAAACGAAAGGAGTGTGTAAGGCTATCGCGGAGCTGTGAGCTTCT 891
 DB 748 TTTATTGAAGAGAGAA-----GTGAGAGAGATTGTGTAAGTGTGTAAGTGTGTAAGTGT 795
 QY 892 GAGAACTGGAAGAGTTGGAGGTGAACAAGTCAACAAGTCAACAAGTCAACAAGTCAACAAGT 951
 DB 796 GAGAGTTTAAAGTAAATTGGAAGTTTAAACAAGAGGGAATTCGCAATGGAATAGAGACT 855
 QY 952 CGATTTCTTGTGTAAGAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1011
 DB 856 AAAATTTCTTTGAAAGAGAGAGATTGGAGATGGAGAGATCTTTGAGTGAATGATTG 915
 QY 1012 GTGGAAGAGTTTCAAGCTTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1067
 DB 916 GCAGAGGAAATTGATAGAACCAATTGAAGAGAGTTTAAAGGTTCTGGTCTTAAATT 971

RESULT 7
 ABZ42036
 ID ABZ42036 standard; cDNA; 981 BP.
 XX

AC ABZ42036;
XX
DT 27-FEB-2003 (first entry)
XX
DE Arabidopsis thaliana gene #20 modulated by PTGS.
XX
DE Posttranscriptional gene silencing; PTGS; plant; transformation; gene;
XX
KW ss.
XX
OS Arabidopsis thaliana.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..981
FT /*tag= a
XX
PN W0200281655-A2.
XX
XX 17-OCT-2002.
XX
XX 05-APR-2002; 2002WO-EP003806.
XX
XX 06-APR-2001; 2001US-0282049P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PA (FRIE-) FRIEDRICH MIESCHER INST.
XX
XX
PI Zhu T, Glazov EA, Meins F, Wang X, Chang H;
XX
XX WPI; 2003-103337/09.
DR P-PSDB; ABP81192.
XX
XX
PT Novel polynucleic acid segment useful for modulating gene expression
PT within a cell by posttranscriptional gene silencing, and for augmenting a
PT plant cell genome.
XX
XX Claim 18; Page 194-195; 438pp; English.
XX
XX The invention relates to a novel isolated polynucleic acid segment
CC modulated within a cell by posttranscriptional gene silencing (PTGS). The
CC invention specifically relates to a method to identify an expression
CC product that is modulated by PTGS. The polynucleotide is useful for
CC modulating the gene expression within a cell by PTGS, by introducing the
CC polynucleic acid into a cell and expressing the nucleic acid segment in
CC the cell to form a product. The polynucleic acid segment is also useful
CC for augmenting a cell genome, and for augmenting a plant genome, by
CC contacting a plant cell with the segment to produce a transformed plant
CC cell, and growing the transformed plant cell to produce a differentiated
CC transformed plant. The sequences shown in ABZ42017 - ABZ42142 represent
CC segments of A. thaliana cDNA modulated by PTGS
XX
SQ Sequence 981 BP; 283 A; 178 C; 228 G; 292 T; 0 U; 0 Other;
Query Match 21.3%; Score 229.2; DB 7; Length 981;
Best Local Similarity 54.9%; Pred. No. 3.8e-62;
Matches 525; Conservative 0; Mismatches 413; Indels 18; Gaps 3;
QY 112 GAAGATGAAGGCTAAGCTGCGAGTCCAGAGATGTTGGATCTCTCTTAAGGAGAGA 171
DB 34 GGAGATGAAGATCGACACAGAAACAGAGCTCTGATCTCTCTCTCTTAAGGAGAA 93
QY 172 GGATGGAGAACTCGTTACCTTTACCTATTCCTAAGGCTTTTGGTCCCAAGCCAAAGATT 231
DB 94 GGTGGTTAGTGAATGAATATGAAATTCAGAGACTTTGGACACACAGCTATTTTA 153
QY 232 CAAGCCATCATGCTTTCCAAAAACATTCCTCCGAAACAGACGCTGCTTCGCC 291
DB 154 CAAGGAATCTTGATCTGCAAAACGCTTTGAAGCTAAAGATTCGACATTATCTCGTC 213
QY 292 ACCATACCTAATCCGTCAGACCTGGCTAAAGCTTTTACTTTTCCATCCCTTAACCT 351
DB 214 ACTAATCCTAATCAGGTACACCTTGGTTAAAGCTCTTGTCTTGTCTCTCCCTTAACCGA 273
QY 352 CACCGGTTTGATCGGTTGCTCGAGTACCAACACCTCTCTTTCACTTCCACCTCAT 411

DB 274 CACAAGTT---TCCAGTTTCTTCTCTGTTACCATCTCTCTCTGTTACCATCCAC 330
QY 412 GACCTTGACCTTTCTTCGAGTACAAGCTTTACGCCAACGGAGATGTTCCGATCTTCG 471
DB 331 CTTCTTGTCCTTCTTGGAAAGGAGTTTACTACGAGTCCCGAGATTT---CGATTCTCC 387
QY 472 GGTCTAGCCAGTCCCAAGAACGTTTCGAACCCACTTTACCGTTTCGGTTCCCTAAAGAAACG 531
DB 388 AGTTTGCTTCTCCAAAGACTGATGACACGACATATGCACTTTTCGCTCCCGAGTCT 447
QY 532 ATCGAGAAACCGGTTGAAAGTCTGTACTTGTGTCGCCGAACCCGTTTTCGACATTCATC 591
DB 448 GTTAAGAGCTGCTCTTGTAAAGATTGTGATTGTTGTAGGAACCCCTTAGGACATGTTTGTG 507
QY 592 TCTTCGTGTCATTACACCAACACATCAAAATCCGAGTCAAGTCCAGTCTTCGTAGAC 651
DB 508 TCCCTATGTCATTTTGGGAAAGAGTAGCTCTCTGAGGAACCGCGGATTTCTTATCGAA 567
QY 652 CAAGCTTTTGATCTGTATTTCGCGGAGTGTATCGGGTTTGGCCCTTTTGGGAACACATG 711
DB 568 AAAGCGGTTGAAGCGTTTGTGAAGGGAAGTTTATAGGTGGACCCCTTTTGGATCATATA 627
QY 712 TTGGGATCTGGAGAGAGCTTTGAAGACACGAGAAAGTCTTCTTTTAAAGGTACGAG 771
DB 628 TTGGAGTACTGTTGATGCAAGCGCGAGAAATCCGAACCAAGGTTCTTGTGTACTTACGAG 687
QY 772 GATCTCAAAGACGACATCGAGACCAACTTGAAGAGCTTGAACCTTTCTTAGAGCTTCT 831
DB 688 GAGCTAAAGACGACACCGAGTTGAGATGAAGCGGATTCGGAGTCTTGGAAATGTGC 747
QY 832 TTCACCGAAGAGAGAAACGAAAGGAGTTGTGAAGGCTATCGCCGAGTGTGTAGCTTC 891
DB 748 TTATTGAAGAAAGAA-----GTGAGAGAGATTGTGAAGTTGTGTAGCTTT 795
QY 892 GAGATCTGAAGACTTGGAGGTGAACAGTCAACCAAGTCGATCAAGAACTTTTCAGAA 951
DB 796 GAGATTTAAGTAATTGGAAGTTAAACAAAGGGAATTCGCAATTCGAATAGAGACT 855
QY 952 CGATTCTTGTTCGGAAGGAGAGTGAAGTATTCGGTTAACTATTTCACCTTCACAA 1011
DB 856 AAACTCTTCTTAGAAAAGGAGAGATTGGAGATGGAGAGATACCTTGAAGTGAATG 915
QY 1012 GTGGAAGATTCTGACCTTAGTGAATGACAGTTAGGTAGTCTGGTCTCACTTT 1067
DB 916 GCAGAGGAATTTGATAGAACCAATTCAGAGAGAGTTTAAAGGTTCTGGTCTTAAAT 971
RESULT 8
AAC42382
ID AAC42382 standard; DNA; 1043 BP.
XX
AC AAC42382;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35341.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN BP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-012182SP.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0135788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127482P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
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PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
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PR 30-APR-1999; 99US-0132407P.
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PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
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PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-015753P.
PR 06-OCT-1999; 99US-0157865P.

PR	07-OCT-1999;	99US-0158029P.	
PR	08-OCT-1999;	99US-0158232P.	
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PR	13-OCT-1999;	99US-0159295P.	
PR	14-OCT-1999;	99US-0159329P.	
PR	14-OCT-1999;	99US-0159330P.	
PR	14-OCT-1999;	99US-0159331P.	
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PR	18-OCT-1999;	99US-0159584P.	
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PR	21-OCT-1999;	99US-0160815P.	
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PR	22-OCT-1999;	99US-0160981P.	
PR	22-OCT-1999;	99US-0160989P.	
PR	25-OCT-1999;	99US-0161404P.	
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PR	25-OCT-1999;	99US-0161406P.	
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PR	28-OCT-1999;	99US-0161920P.	
PR	28-OCT-1999;	99US-0161931P.	
PR	29-OCT-1999;	99US-0162142P.	
Query Match			
Best Local Similarity 21.3%; Score 229.2; DB 3; Length 1043;			
Matches 525; Conservative 0; Mismatches 413; Indels 18; Gaps 3;			
QY	112	GAGATCAAGCGCTAAGCTCGGATCCAGAGATGTTGGATCTCTCTCTTAAGGAGAGA	171
DB	96	GGAGTGAAGATCTGACACAAAGAAACAAAGACTCTGATCTCTCTCTCTTAAGGAAA	155
QY	172	GGATGGAGAACTCGTTACCTTTTACTATTCCTCAAGGGTTTTGGTCCCAAGCCAAAGATT	231
DB	156	GTTTGGTTAGTGAAGTAAATATGAAATTCAGGACTTTGGCACACACAAAGCTATTTTA	215
QY	232	CAAGCATCATGCTTTTCCAAAACATTTCAATCCCTCGAAACAGCGTCTCTTCGCC	291
DB	216	CAAGGAATCTGTGATCTCCAAAACCGCTTTGAAGCTAAAGATTCCGACATTTATCCTCGTC	275
QY	292	ACCATACCTAAATCCGGTACAACTCGCTAAAGCTTTAACTTTACCATCCTTTAAACCGT	351
DB	276	ACTAATCTTAATCAGTACCACCTTGGTTAAAGCTCTTCTCTTTGCTCTCTTAACCGA	335
QY	352	CACCGTTTGTATCCGGTTGCTCGAGTACCAACACACCTCTTTTCACTTCCAAACCTCAT	411
DB	336	CACAAAGTT--TCCAGTTTCTTCTCTGTGAACCATCTCTCTGTGTCCACCAATCCACAC	392
QY	412	GACCTGTACCTTCTTCGAGTACAACTTTAAGCTTAAGCTTAAGCTTTCGGATCTCTCG	471
DB	393	CTTCTGTGCGCTTCTTGGAAAGGATTACTACAGTCCCGAGATT--CGATTTCTCC	449
QY	472	GGTCTAGCCAGTCCAAAGACGTTCCGAAACCACTTACCGTTCCGTTCCCTTAAGGAAAG	531
DB	450	AGTTTGTGCTTCTCAAGACTGATCAACACGCACATATCGCATCTTTCTGCTCCCGAGTCT	509
QY	532	ATCCAGAAACCGGTGTGAAGTCTGTACTTGTGCGGAAACCGGTTTGAACATTCATC	591
DB	510	GTTAAGAGCTCGCTCTGTGAAGATTGTGTATTTGTGTAGGAACCCCTAAGGACATGTTTGTG	569
QY	592	TCTTCGTGGCATTACACCAACATCAATCCAGTCAAGTCAAGTCCAGTCTTGTAGAC	651
DB	570	TCCTATTGGCATTTTGGAAAAAGCTAGCTCCTGAGGAACCGCGGATTATCTATCGAA	629
QY	652	CAAGCTTTTGATCTGTATNTGCCGGGAGTGATCGGGTTTGGCCCGTTTGGGAACATG	711

DB	630	AAAGCGTTGAAGCGTTTTTGTGAAGGAAGTTTATAGTGGACCCCTTTTGGGATCATATA	689
QY	712	TTGGGATACTCGAGAGAGCTTTGAAGACCCAGAGAAAGTCTTCTTTTAAAGGTACGAG	771
DB	690	TTGGAGTACTGTGTATGCAAGCGCGAGAAATCCGAACAAGGTCTTGTGTACTTACGAG	749
QY	772	GATCTCAAGACGACATCGAGACCAACTTTGAAGAGGCTTGAACACTTTCTTAGAGCTTCT	831
DB	750	GAGCTAAAGACGACAGCGAGTTGAGATGAAGCGGATTCCTTGAATGTGC	809
QY	832	TTTACCGAAGAGAGAGAAAGGAGTTGTGAAGGCTATCGCGAGCTGTGTAGCTTC	891
DB	810	TTTATTGAAGAAGAA--GTGAGAGAGATTGTGAAGTTGTGTAGCTTT	857
QY	892	GAGAATCTGAAGAAGTTGGAGGTGAACAAGTCAACAAGTCGATCAAGAACCTTTGAGAAT	951
DB	858	GAGAGTTTAAGTAAATTTGGAAGTTAACAAGNAGGAAATTCGCAAAATGAATAGAGCT	917
QY	952	CGATCTCTTTTCGAAAGGAGAGAGTGAATGGGTTAACTATTGTACCTTCAACA	1011
DB	918	AAAACCTTTCTTTAGAAAAGGAGAGATTGGAGATCGAGAGATACCTTGAAGTGAATG	977
QY	1012	GTGGAAGATTCTCAGCCTTAGTGGATGACAGTTAGGTGGATCTGGTCTCACTTT	1067
DB	978	GCAGAGAAATGTAGAACCAATTGAGAGAGTTTAAAGGTTCTGGCTTAAAT	1033

RESULT 9

ABZ13222

ID ABZ13222 standard; DNA; 996 BP.

XX ABZ13222;

AC ABZ13222;

XX 21-JAN-2003 (first entry)

DT 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 1027.

DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX Arabidopsis thaliana.

XX Arabidopsis thaliana.

XX Arabidopsis thaliana.

XX WO200216655-A2.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US026685.

XX 24-AUG-2000; 2000US-0227866P.

XX 26-JAN-2001; 2001US-0264647P.

XX 22-JUN-2001; 2001US-0300111P.

XX (SCRI) SCRIPPS RES INST.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

XX Identifying a stress condition to which a plant cell has been exposed and

XX producing plants with increased tolerance to these abiotic stresses.

XX Claim 144; SEQ ID NO 1027; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant

XX cell has been exposed, comprising: (a) contacting nucleic acid

XX representative of expressed polynucleotides in the plant cell with an

XX array or probes representative of the plant cell genome; and (b)

XX detecting a profile of expressed polynucleotides in the plant cell

XX characteristic of a stress response. The method is useful in the

XX production of transgenic plants, cells and seeds and in producing plants

XX with increased tolerance to abiotic stress. The present sequence is that

XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used

CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 996 BP; 306 A; 199 C; 213 G; 278 T; 0 U; 0 Other;

Query Match 20.4%; Score 219.2; DB 6; Length 996;
Best Local Similarity 53.0%; Pred. No. 6.1e-59;
Matches 520; Conservative 0; Mismatches 453; Indels 9; Gaps 2;

QY 86 AAACCTCGGAGTCCGAAAGCCGGAAGAGATGAAGGCTAAGCTGGAGTTCCAAAGAGA 145
DB 17 AAGCTCATCCTTCCAAACTACATGAAGAGAGCAACGTTAGTCAAGAAACCAAGAACT 76

QY 146 TGTGGATTCTTCCCTAAGAGAGAGATGGAGAACTCGTTACCTTTACTTCTTCCAAG 205
DB 77 TGATCACTTCTTACCTTCAGACAAAGATTTCATGGGTATGGTCTCTCAACTTACAAG 136

QY 206 GGTTTTGTGTCGAAGCCAAAGAGATTCAAGCCATCATGTCTTCCAAAAACATTTCCAAT 265
DB 137 GTTGTGGTACTATCCAAACACACTCCAAGCGTCTTGAGCTCCAAAAACACTTCAAGC 196

QY 266 CCCTCGAAAGACAGCTGTTCTCGCCACCATACCTTAATCCGGTACAACTGGCTTAAAG 325
DB 197 CACGAGATACATGATATATCTCTGCTTCTTGGCCAAAGGTGGAAACCATTTGGCTCAAT 256

QY 326 CTTTAACTTTCACCATCCTTAACCGTCAACCGTTTGATCCGGTTCCTCGAGTACCAAC 385
DB 257 CCTTAATTTTCGTTGTGATATAGAGAAAGT-----ACCGGGAACCCCTCAACAC 310

QY 386 ACCCTCTTTTCACTTCCAAACCTCATGACCTTGACCTTTCTTCGAGTACAAGCTTTACG 445
DB 311 ATCCTTTGCTCTTCAAAACCCCTCATGACCTTGTCCTTCTTTCGAGTTGAGTTATACG 370

QY 446 CCAACGAGATGTTCCGATCTCTCGGCTAGCAGTCCAGAACCTTCGCAACCCACT 505
DB 371 CTAATAGCAAAATTCGGATCTCGAAGATATCTTCTCTATGATCTTTCTTCTACACA 430

QY 506 TACCGTTGCTTCCCTAAGGAAACGATCGAAGAACCCGGTGTGAAGCTCGTGACTTGT 565
DB 431 TGCACCTTACAAGCTTGGTGAAGCCACCAAAA---GCTTGCAAAACCGTATATGTGT 487

QY 566 GCCGGAACCCGTTTGACATCTCTCTCGTGGCATACCAACCAATCAATCCG 625
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DT 17-OCT-2000 (first entry)
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DT 17-OCT-2000 (first entry)

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Hybridisation assay; Genetic mapping; Gene expression control;
protein identification; signal transduction pathway; metabolic pathway;
promoter; termination sequence; ss.

Arabidopsis thaliana.

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PR 26-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 28-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 18.6%; Score 200.8; DB 3; Length 1212;
Best Local Similarity 53.0%; Pred. No. 5.1e-53;
Matches 514; Conservative 0; Mismatches 432; Indels 24; Gaps 3;

QY 104 AAGCGAAGAAGATCAAGGGCTAAGCTCGAGTTCAGAGATGTCGAGATGTCGAGATGTCGATTCCTTCTTA 163
Db 71 AAGAGAAGAGAAGAAACCAAGTGAAGAAACCAAGTTGATCTCTTCACTTCCTT 130
QY 164 AGGAGAGAGATGGAGAACTCGTTACCTTTACCTTATTCCTTCAAGGGTTTGGTGCAAGCCA 223
Db 131 CAGACATAGATTGCTCAGGGACCAAGTTGTACAAGTACCAAGGATGTTGGTACGACAAAG 190
QY 224 AAGAGATTCAAGCCATCATGTCCTTTCCAAACATTTCCATCCCTCGAAGAACGACGTCG 283
Db 191 ATATTCTCCAAGCAATCTCTCAATTTCAACAAAAAATTTTCAGCCCAAGAAACGGATATAA 250
QY 284 TTCTCGCCACCATACCTAAATCCGGTACAACTCGGTAAAGCTTTAACTTTCCACCATCC 343
Db 251 TTGTTGCTTTCTTTCCCAATCGGTAGACTTGGCTCAAGGCACTCACATTCGACTCG 310
QY 344 TTAACCGTCACGGTTTGATCCGGTTGCTCGAGTACCAACCCCTCTTTTTCATTCCA 403
Db 311 CGCAAG-----ATCAAAACACACTTCAGACAATCATCTCTTGTAACTCAT 358
QY 404 ACCCTCATGACCTTGTTACCTTTCTTCGAGTACAGCTTTACGCCCAAGGAGATGTTCCCG 463
```

359	ATCCTCATGAGCTAGTGC	CGCGTACCTCGAGCTCGATCTTTATCTCAAAAGAGCTCAAAACCGG	418	25-MAR-1999;
				99US-0126264P;
				99US-0126785P;
464	ATCT-----CTCGGCTAGCCAGTCC	CAAGAACGTTCCGCAACCCCACTTACCGTTCGGTT	517	29-MAR-1999;
				99US-0127462P;
				99US-0128234P;
419	ATTTGACCAAGTTGCCATCATCTCCGAGATTGTTCTCAACCCACATGTCCTCTTGATG	478	01-APR-1999;	
				99US-0128714P;
				99US-0129845P;
518	CCCTAAAGGAAACGATCGAGAAACCCGGTGTGAAGTGCTGTTGACTGCTGTCGCGGAAACCCGT	577	06-APR-1999;	
				99US-0130077P;
				99US-0130409P;
479	CGCTTAAAGTACCGTTCAAGAGTCCCTTGC	CAAGATCCGTGTACGTGTGCAGGAACGTGA	538	16-APR-1999;
				99US-0130510P;
				99US-0130891P;
				99US-0130891P;
578	TTGACACATCTACTCTTCGTGTCATATACACCAACCAACATCAAAATCCGAGTCACTGAGCC	637	21-APR-1999;	
				99US-0131449P;
				99US-0132048P;
539	ATGACGTATTGATATACATTGTGTGTTT	CGAAATCTCCATGA-----GTGGAGAAACA	592	30-APR-1999;
				99US-0132407P;
				99US-0132485P;
638	CAGCTCTTGTAGACCAAGCTTTT	GATCTGTATTCGCCGGGAGTGATCGGGTTGGCCCGT	697	04-MAY-1999;
				99US-0132486P;
				99US-0132487P;
593	ATTTAAGTCTCGAGGCTTTGTTTCGAGTCTTTATGTAGCGGAGTTAACTTATGCGGTCCCT	652	06-MAY-1999;	
				99US-0132863P;
				99US-0132863P;
698	TTTGGGAACACATGTTGGGTACTCGAGAGAGAGCTTGAAGACACAGAGAAAGTCTTCT	757	11-MAY-1999;	
				99US-0134218P;
				99US-0134218P;
653	TATGGGAAAATGTTTAGGCTATTTGGAGAGGAAGCTTGAAGATCCCTTAAGCATGTGCTTT	712	14-MAY-1999;	
				99US-0134221P;
				99US-0134370P;
758	TTTTTAAGGTACGAGGATCTCAAAGA	CGACATCGAGACCAACTTTGAAGAGGCTTGCACATT	817	14-MAY-1999;
				99US-0134370P;
				99US-0134768P;
713	TCCTGAGTACGAGGAGTTCAAGACGCGCTCGTGTGCAAAATCAAGAGACTTTGCAGAGT	772	18-MAY-1999;	
				99US-0134941P;
				99US-0135124P;
818	TCCTAGAGCTTCCTTTCAACGAAGAGAGAA	CGAAGGAGTTGTGAAGGCTATCGCG	877	20-MAY-1999;
				99US-0135353P;
				99US-0135629P;
773	TCCTAGATTTCCTTCAAGAAACCTTAGCGGTTGGAGATCAACAAACAGGAAGCTTGTG	832	24-MAY-1999;	
				99US-0136021P;
				99US-0136392P;
878	AGCTGTCTAGCTTCGAGAACTCGAAGTCTGAAGAGTTGGAGGTGAACAACTCAACAAAGTCCGATCA	937	27-MAY-1999;	
				99US-0136782P;
				99US-0137222P;
833	AACCTTTGCTTCTAAGAAACCTTAGCGGTTGGAGATCAACAAACAGGAAGCTTGTGCG	892	01-JUN-1999;	
				99US-0137528P;
				99US-0137528P;
938	AGAACTTTGAGAAATCGATCTCTGTTTCGAAAGGAGAGTGAAGTGATTTGGTTAACTATT	997	04-JUN-1999;	
				99US-0137724P;
				99US-0138094P;
893	AAGGAGTAAGTTTCAAGAGTTTTTTCGTTAAAGGGGAAGTTGGTGATTGGAAGAGTTATA	952	07-JUN-1999;	
				99US-0138447P;
				99US-0138540P;
998	TGTCACCTTCAAGTGGAAAGATTGTACGCCTTAGTGGATGACAAAGTAGGTGGATCTG	1057	10-JUN-1999;	
				99US-0138840P;
				99US-0139119P;
953	TGACTCTCTGAATGGAACAAACAAATCGACATGATTTGTGGAGGAACACTTCAAGGCTCTG	1012	14-JUN-1999;	
				99US-0139452P;
				99US-0139453P;
				99US-0139492P;
1058	GTCTCACTTT	1067	16-JUN-1999;	
				99US-0139454P;
1013	GTITGAATTT	1022	17-JUN-1999;	
				99US-0139455P;
				99US-0139456P;
				99US-0139457P;
				99US-0139458P;
				99US-0139459P;
				99US-0139460P;
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				99US-0139750P;
				99US-0139750P;
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				99US-0139817P;
				99US-0139899P;
				99US-0139899P;
				99US-0140353P;
				99US-0140354P;

PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144632P.
PR 21-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145132P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 13-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0149368P.
PR 16-AUG-1999; 99US-0149175P.
PR 17-AUG-1999; 99US-0149426P.
PR 18-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151666P.
PR 27-AUG-1999; 99US-0151680P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 01-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 22-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.

PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 14-OCT-1999; 99US-0159329P.
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PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159684P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 22-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 18.0%; Score 194.2; DB 3; Length 1205;

Best Local Similarity 52.6%; Pred. No. 6.5e-51;

Matches 508; Conservative 0; Mismatches 433; Indels 24; Gaps 3;

QY 109 GAAGAAGATGAAGGCTTAAGCTCGAGTTCCAAGAGATGTTGGATTCTCTTCTTAAGGAG 168
DB 64 GAAGAGAGAGAAACCAAGTGAAGATTCGAAGATTTGATCTCTTCACTTCTTCAAC 123
QY 169 AGAGATGGAGAACTCGTTTACCTTATCCAAAGGTTTGGTGCCAAAGCCAAAGAG 228
DB 124 ATAGATTGCTCTGGGACCAAGTTGTACAAAGTATCAAGGATGTGTGACGATAAAGACATT 183
QY 229 ATTCAAGCCATCATGTCTTTCCAAACATTTCCAAATCCCTCGAAAGGAGTGGTCTC 288
DB 184 CTCGAAGCAATCCTCAAAATCAACAAATCTTTGAGCCCAAGAAACCGATATATTTT 243
QY 289 GCCACCATACCTAAATCCGGTACAACTGGGTAAAGCTTTAACTTTCCACATCCTTAAC 348
DB 244 GCTTCTTTCCCAATCAGGTACGACTTGGCTCAAGGCACCTCACATTGCGACTCGCTCAA 303
QY 349 CGTCACCGTTTGATCCGGTTGCGCTCGAGTACCAACACCTCTTTTCACTTCCAAACCT 409
DB 304 AGATCAAAACATCTTCAG-----AAAATCATCTCTGCTAACTCATATCTCT 351
QY 409 CATGACCTTGTAACCTTTCTTCGAGTACAAGCTTTTACGCCAACAGGAGATGTTCCCGATCTC 468
DB 352 CATGAGCTAGTGGCGTACTCGAGCTCGATCTTTATCTCAAAAGCTCGAAACCGGATG 411
QY 469 TCGGGTCT-----AGCCAGTCCAAAGAGCTTCCGAAACCCACTTACCGTTGGTTCCTTA 522
DB 412 TCCAAGTTACCATCATCTCCGAGATGTTCTCAACCCACATGCTTTTCGATCGCGCTT 471
QY 523 AAGGAACGATCGAGAAACCGGTTGGAAGTCTGTGCTGTACTTGTGCGCGAACCCGTTTGCAC 582
DB 472 AAAGTACCAATGAAGGAGACTCTTGGCAAGATGATGATGTGTGCAAGAACGTAAGAAC 531
QY 583 ACATTCATCTCTCGTGGCAATTACCAACAACTAAATCCGAGTCAAGTCAAGCCCAAGTC 642
DB 532 GTGTGGTATCACTTTGGTGTTCGAAACCTCCATTAGTGGAGAA-----ACAATTTA 585
QY 643 TTGCTAGACCAAGCTTTTGATCTGATTTGCGGGGAGTGATCGGGTTGGCCCGCTTTGG 702

586	AGTCTCGAGGCTTTGTTGCAGTCTTTATGTAGCGGAGTTAACTTTATGCGGTCCTCTGTGG	645
703	GAACACATGTTGGATACTCGGAGAGAGAGCTTGAAGAGACCAGAGAAAGTCTTCTTTTTTA	762
646	GAAATGTGTTAGGCTATTGGAGAGGAAGCTTGGAAAGTCCCTAAGCATGTGCTTTTCTTGG	705
763	AGGTACGAGAGTCTAAAGACGACATCGAGACCAACTTGAAGAGGCTTGGCACTTTCTTA	822
706	AGGTACGAGAGTGAAGACGGAGCCTCGTGTGCAAACTCAAGAGAGCTTGCAGAGTCTCTTA	765
823	GAGCTTCTCTTACCCGAAGAAGAGGAAACGAAAGCGAGTTGTGAAAGCTATCGCCGAGCTG	882
766	GATTTTCCATTCAAAAGNAGAAAGATGATGTGGAGGTGTAGCAAGATCTTGGAACTT	825
883	TGTAGCTTCGAGAACTGAAGAAAGTTGGAGGTGAAACAAGTCAAAAGTCGATCAAGAAC	942
826	TGTTCTCTAAGAAACCTTTAGCGCTTTGGAGATCAACAAGACAGGAAGCTTGTCCGAAGGA	885
943	TTTGAGAAATCGATTCTTTGTTTTCGGAAGGAGAGTGCAGTCAATTTGGGTAACTATTGTCA	1002
886	GTAAGTTTCAAGAGTTTTTTCCGTAAAGGGAAGTTGGTGATTTGGAAGATTATATGACT	945
1003	CCTTTCAAGTGGAAAGATTGTGAGCCTTAGTGGATGACAAGTTAGGTGGATCTGGTCTC	1062
946	CCTGAAATGAAAACAAACAAATCGACATGATGTTTGGAGAGAAACTTCAAGGCTCTGGTTTG	1005
1063	ACTTT	1067
1006	ATATT	1010

RESULT 13	
AA054410	
AA054410	standard; cDNA; 1400 BP.
XX	
XX	
AA054410;	
XX	
XX	
17-JUN-2003	(first entry)
XX	
XX	
DE	Lolium perenne defensin e (LpDeFe) cDNA.
XX	
XX	
KW	Ryegrass; thionin; TH; thaumatin-like protein; TL; defensin; DEF; ER;
KW	elicitor-responsive protein; disease resistance; plant defence response;
KW	protein storage; pest resistance; genetic marker; gene therapy; antipept;
KW	agricultural; LpDeFe; gene; ss.
XX	
XX	
OS	Lolium perenne.
XX	
Key	Location/Qualifiers
FT	CDS 153..833
FT	/*tag= a
FT	/product= "Ryegrass DeFe (LpDeFe) protein"
XX	
XX	
PN	WO200288359-A1.
XX	
XX	
PD	07-NOV-2002.
XX	
XX	
PP	01-MAY-2002; 2002WO-AU000539.
XX	
PR	02-MAY-2001; 2001AU-00004735.
XX	
XX	
PA	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA	(AGRE-) AGRESEARCH LTD.
XX	
PI	Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX	
XX	
DR	WPI; 2003-201227/19.
DR	P-PSDB; AAE35947.
XX	
PT	New ryegrass or fescue nucleic acid encoding a thionin, thaumatin-like,
PT	elicitor-responsive or defensin polypeptide, for modifying disease and/or
PT	plant resistance, plant defence response and/or protein storage in a
PT	plant.

Db 1030 CAGGAATGGGACGGTGGCGGATTTGGGCAACACCACTGACCCAGAGATGGGCACAAGTT 1089
Qy 1023 GTACAGCTTTAGTGATGACAGTTAGTGGATCGTCTCACATT 1067
Db 1090 GGATGGATCGTCAGGAGAGCTCAAAGGTTTCGGCCCTCGCCTT 1134
RESULT 14
ADD25213/c
ID ADD25213 standard; DNA; 271990 BP.
XX AC ADD25213;
XX AC 15-JAN-2004 (first entry)
DT XX Fertility restorer protein genomic DNA sequence.
DE XX fertility restorer protein; male sterile plant; viable pollen production;
KW XX selection marker; ds; gene.
KW Unidentified.
XX OS WO2003006622-A2.
XX PN 23-JAN-2003.
XX XX 12-JUL-2002; 2002WO-US022217.
XX PR 12-JUL-2001; 2001US-0305026P.
XX PR 13-JUL-2001; 2001US-0305363P.
XX PR 30-JUL-2001; 2001US-0308736P.
XX XX (UWMC-) UNIV MCGILL.
XX PA (DNAL-) DNA LANDMARKS INC.
XX XX Brown GG, Formanova N, Dendy C, Landry BS, Cheung W, Jin H;
XX WPI; 2003-221734/21.
XX XX New nuclear fertility restorer genes, useful for restoring fertility in
PT cytoplasmic male-sterile plants such as Brassica napus plants, or for
PT increasing production of viable pollen in a plant.
XX Claim 1; SEQ ID NO 87; 191pp; English.
XX PS The invention comprises the amino acid and coding sequences of isolated
CC fertility restorer proteins. The DNA and protein sequences of the
CC invention are useful for restoring fertility in male sterile plants, such
CC as Brassica napus plants. The DNA and protein sequences of the invention
CC are useful for increasing production of viable pollen in a plant. The DNA
CC and protein sequences are also useful as selection markers to identify
CC transformed plant cells. The present genomic DNA sequence contains coding
CC sequences for fertility restorer proteins of the invention.
XX SQ Sequence 271990 BP; 89597 A; 47325 C; 46930 G; 88078 T; 0 U; 60 Other;
Query Match 17.1%; Score 184.2; DB 9; Length 271990;
Best Local Similarity 53.5%; Pred. No. 1.8e-46;
Matches 485; Conservative 0; Mismatches 403; Indels 19; Gaps 4;
Qy 114 AGATGAAGGCTAAGTGGCGAGTTCACAGAGATGTTGGATTCTCTCTTAAGGAGAGAGG 173
Db 244850 AGACGCAAGATAAGTGAAGAAACCAAGGAGGATCTCTCTGCTCTTCACACACAGA 244791
Qy 174 ATGGAGACTCGTTACTCTTACCTATTCCAGGGTTTGGTCCCAAGCCAAAGAGATTCA 233
Db 244790 TTACCAGGGCAFAAGATTGTAAATATCAAGGATGTTGGTATTATTAACACACCTCCA 244731
Qy 234 AGCCATCATGCTTTCCAAAACATTTCCATCCCTCGAAACAGAGTGGTCTCGCCAC 293
Db 244730 AGGTGTC-TCAATTCAGAGAGGTTTTCACCGGAGACATGATGTAATCATTTGCTTC 244672
Qy 294 CATACTAAATCCGGTACACCTGGCTGCTAAAAGCTTTAACTTTACCATCTCTTAACCGTCA 353

Db 244671 GTACCCCAATCAGGCACTACTTGGCTCAAGCCCTCAGTCGCTCTGCTTGAAGATC 244612
Qy 354 CCGGTTTGATCCGGTTGGCTCGAGTACCAACACACCTCTTTTCACTTCCAAACCTCATGA 413
Db 244611 AAAGAACCACCTCTCTG-----ATCATCTCTCTATATCATATCTCTCATGG 244564
Qy 414 CCTTGTAACCTTTCTTCGAGTACAAGCTTTACGCCAACGAGATGTTCCGATCT---CTC 470
Db 244563 CATTTACCATTTCTTTGGAGATCGATGTGTACCAAGAAAGCTCAAGTCTCTTAAGCCCAA 244504
Qy 471 GGGTCTAGCCAGTCCAAGAAACGTTCCGAACCCACATTACCGTTTCGGTTCCCTAAAGGAAC 530
Db 244503 GTTCTCAGCACCTCCGAGGCTGTTCTCGACTCACATGCCACATGCCACGAAGC 244444
Qy 531 GATCGAGAAACCGGTTGAGAGTCTGTACTTGTGCGGAAACCCGTTTGAACATTTAT 590
Db 244443 ACTCAAGCACTCTCTCTGCAAGATTGTGTACGTGTGCAAGAAACGTTGAAGGACACGTTGAT 244384
Qy 591 CTCCTCGTGGCATTAACCAACCAACATCAAAATCCGAGTCAGTGAGCCAGTCTTCTCTAGA 650
Db 244383 CTCGTGTTGGTTTACAGCTGTGCTATATATAAATCCAAACCAACAGAGTCTCTCGA 244324
Qy 651 CCAAGCTTTTGATCTGTATTCGCGGGAGTGTATCGGGTTTGGCCGTTTGGGAACACAT 710
Db 244323 GTCTATGTTTAAACGAGTTCTCGATGGAACCAACTATTATTGGACCTTTTGGGATCATCT 244264
Qy 711 GTTGGGATCTGGAGAGAGCTTGAAGAGACCAAGAGAACTCTCTTTTAAAGGTAGA 770
Db 244263 CTTGAGTTACTGGAGAGAACTTGGAAAGACCAAGCATGTCTCTTTTCATGAGGTAGA 244204
Qy 771 GGATCTCAAGACGACATCGAGACCAACTTGAAGAGGCTTGCACATTTCTTTAGAGCTTCC 830
Db 244203 GGAGATGAAGCCGAGCCTCGTATCAGATCAAGAGACTTCTGGGATGTC 244144
Qy 831 TTTCCACCAAGAGAGGAAACGAAGGAGTGTGTAAGGCTATGCCCGAGCTGTGTAGCTT 890
Db 244143 TTTTACTAAGCAAGAAAGATAGTGGATCTGTGACGGGATCTTGGACCTCTGCTCTCT 244084
Qy 891 CGAGAACTGAAGAGATTGGAGGTGAACAAGTCAAAAGTCGATCAAGAACTTTTGAGAA 950
Db 244083 CGGTAATCTGAGCAGTTTGGAGGCTAACAA---AACAGGACAATAACATATGAGGACA 244027
Qy 951 TCGATCTTGTTCGAAAGGAGAGAGTGTGATGGTTAACTATTGTCACTTCACTTCA 1010
Db 244026 CAAGTTTTTTTTTCCGTAAGGAGAGTCCGTGACTCGAAAAATTTATCTAGCTCTGAAT 243967
Qy 1011 AGTGGAA 1017
Db 243966 GGAGAAA 243960
RESULT 15
ABZ68951
ID ABZ68951 standard; DNA; 1017 BP.
XX AC ABZ68951;
XX AC 28-MAY-2003 (first entry)
DT XX Nucleotide sequence of desulfoglucosinolate sulfotransferase AtST5a.
DE XX Plant; desulfoglucosinolate sulfotransferase; AtST5a; AtST5b; AtST5c;
KW glucosinolate; transgenic plant; gene; ss.
KW Arabidopsis thaliana.
XX OS
XX Key Location/Qualifiers
FT CDS 1..1017
FT /*tag= a
FT /product= "desulfoglucosinolate sulfotransferase AtST5a"
XX PN WO2003010318-A2.

XX PD 06-FEB-2003.
XX XX 24-JUL-2002; 2002WO-CA001144.
XX PF
XX XX 24-JUL-2001; 2001US-0307141P.
XX PR
XX XX (UYCO-) UNIV CONCORDIA.
XX PA
XX PI Varin L, Spertini D;
XX XX WPI; 2003-248082/24.
XX DR P-PSDB; ABP72962.
XX XX
PT Novel isolated or purified polypeptide having biological activity of
PT desulfoglucosinolate sulfotransferases, useful as enzymes involved in
PT glucosinolate biosynthesis in transgenic plants.
XX XX
PS Claim 9; Page 54-55; 68pp; English.
XX XX
CC The present sequence encodes a plant desulfoglucosinolate
CC sulfotransferase, designated AtST5a. The specification also describe
CC AtST5b and AtST5c. AtST5a and AtST5b are constitutively expressed in all
CC parts of the plants, while AtST5c does not seem to be expressed in the
CC early stage of development. These enzymes are involved in glucosinolate
CC synthesis in plants. The desulfoglucosinolate sulfotransferase
CC polynucleotides are useful for modulating glucosinolate biosynthesis in
CC transgenic plants
XX XX
SQ Sequence 1017 BP; 296 A; 205 C; 240 G; 276 T; 0 U; 0 Other;

Query Match 16.2%; Score 174.4; DB 7; Length 1017;
Best Local Similarity 52.6%; Pred. No. 1.3e-44;
Matches 494; Conservative 0; Mismatches 416; Indels 30; Gaps 4;

QY 134 AGTTCGAAGAGATGTTGGATCTCTTCTTAAGGAGAGAGGATGAGAACTCGTTA---CC 190
DB 71 AGTATCAAGATTTTCATCGCTACACTTCCAAAGAGCAAAAGGCTGGAGACCATGAGATCT 130
QY 191 TTTACCTATTCCAAAGGTTTGTGGCCAAAGAGATTCAAGCCATCATCTCTTTCC 250
DB 131 TAACCCATAGCTGGACACTGTGGCAAGATGTCTCTCGAAGTCTTTTTCACGCTA 190
QY 251 AAAAACAATTTCCAAATCCCTCGAAACGAGCGTGTCTCGCCACCATCTAAATCCGGTA 310
DB 191 AAGACCATTTTGAAGACGACCAACTGATTTCTCTCGTCTGTAGTACCCCAAAACCCGGTA 250
QY 311 CAACCTGGCTAAAGCTTTAACTTTTCACTTCCATCCCTTAACCGTTCACCGGTTGATCCGGTTG 370
DB 251 CAATGTGGCTCAAGACACTAACTTACCGATTCGCAATCGTTCGTTTCGTACGACGACG--- 307
QY 371 CCTCGAGTACCACACCCCTCTTTTCTACTTCCAAACCTCATGACCTTTGTACCTTTCTTCG 430
DB 308 -----CGCAAAACCCACTCTCTCAAAACGAAACCCCTCACGAGTTGTCCCTTACGTTG 358
QY 431 AGTACAGCTTTAGCCCAACGAGATGTTCCCGATCTCTCGGTCCTAGCCAGTCCAGAA 490
DB 359 AGATCGACTTCGCGTTTACCCCAACCGGTTGATGTTCTTCAAGACAGAAAGAACCC---AC 415
QY 491 CGTTTCGAACCCACTTACCGTTTCGTTTCCCTTAAAGAAACGATCGAGAAACCCGGTGTGA 550
DB 416 TTTTCTCTACTCATATCCAAACGGTTATTACCCGATTCGATGTCGAATCTCTGGTTGTA 475
QY 551 AGGTCGTGTACTGTGCGGAAACCGGTTTGACATTCATCTCTCTCGTGGCATACACCA 610
DB 476 AGATGGTGTACATATGGAGAGACCCGAAAGATATTTTCATCTCCATGTGGACTTTCTTAC 535
QY 611 ACAACATCAAAATCCGAGTCACTGAGAGCCCGAGTCTTGTGACCAAGCTTTTGTATCTGATT 670
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DB 596 GTAAAGGTTTATCTGTGTATGGTCTTTATCTGGATCAATGTTTGGGTTATTTGGAAGCTT 655
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QY 791 AGACCAACTTGAAGAGGCTTGCACCTTTCTTTAGAGCTTCTTTTCCACCGAAGAGAGAAC 850
DB 716 TGCCTTTTGTGAGAGATTTGGCTGAGTTTCATGGGTTATGGATTCTACTGATGAGGAAGG 775
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DB 836 AAGCTTAACAAGGTGATATAAAGAAAGAGAGGATCGTCTGCTGTTTATGCGAATAGCGGT 895
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DB 896 ATTTTAGGAAAGGAAAGGTTGGAGATTGGGCTAATTTATTTGACTCTCTGAGATGGCTCTC 955
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DB 956 GTATTGATGGCTTTAGTGGAGGAGAAATTCAAAGATACTGG 995

Search completed: August 17, 2004, 02:59:48
Job time : 498 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2004, 02:43:04 ; Search time 3226 Seconds

(without alignments)
9969.488 Million cell updates/sec

Title: US-10-019-931-1

Perfect score: 1077

Sequence: 1 atggctacacccaagcatgaa.....gttcacttcagggtgagc 1077

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gssrl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541.4	50.3	811	28	BH733391
2	530	49.2	757	28	BZ062934
3	494.6	45.9	671	9	AU238005
4	486	45.1	574	9	AV827990

5	486	45.1	635	14	CB260303
6	484	44.9	523	9	AV442770
7	485	43.2	641	9	AV520946
8	462	42.9	585	14	CB260353
9	462	42.9	638	9	AV441110
10	453.6	42.1	727	14	CD837475
11	435.6	40.4	734	14	CD834047
12	421.4	39.1	531	9	AV442439
13	400.2	37.2	551	14	CD833738
14	367.2	34.1	657	14	CD822905
15	365.8	34.0	760	29	CC952179
16	365.6	33.9	566	14	H76376
17	363	33.7	379	14	CB257253
18	348	32.3	416	9	AV810198
19	346.2	32.1	643	9	AV441090
20	341.4	31.7	534	14	N65491
21	325	30.2	411	9	AV520947
22	317.8	29.5	479	14	T43254
23	305	28.3	341	9	AV442113
24	304.6	28.3	372	14	T13626
25	299.2	27.8	426	28	BH213349
26	296.8	27.6	373	14	T13706
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28	276.8	25.7	416	14	N37700
29	264.6	24.6	361	28	BH580029
30	263	24.4	698	13	BU831310
31	259.6	24.1	738	14	CF418052
32	257.2	23.9	795	14	CA799562
33	253	23.5	694	13	BU834467
34	249.6	23.2	781	14	CA782758
35	243.4	22.6	680	14	CB006702
36	238.8	22.2	329	14	T43998
37	238	22.1	739	28	BZ478554
38	237	22.0	475	14	T44617
39	230.2	21.4	353	14	T44081
40	228.8	21.2	406	9	AU229130
41	227.8	21.2	792	14	CA922564
42	221.4	20.6	701	14	CF509356
43	221.2	20.5	934	29	CG919663
44	220.4	20.5	580	10	BE942160
45	219	20.3	402	28	BH756209

ALIGNMENTS

RESULT 1
BH733391
LOCUS BH733391
DEFINITION BOMIU60TR BO_2_3_KB Brassica oleracea genomic clone BOMIU60,
811 bp DNA linear GSS 20-FEB-2002
ACCESSION BH733391
VERSION BH733391
KEYWORDS genomic survey sequence.
SOURCE BH733391.1 GI:18838786
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
1 (bases 1 to 811)
AUTHORS Whole genome shotgun sequencing of Brassica oleracea
TITLE Unpublished (2001)
JOURNAL
COMMENT Other_GSSs: BOMIU60TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

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FEATURES
  source
    Location/Qualifiers
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        /clone_lib="BO_2_3_KB"
        /notes="vector: pHO51; Site 1: BstXI; 2-3 kb sheared
        genomic DNA inserted into pHO51 using BstXI linkers"

ORIGIN
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  Best Local Similarity 84.6%; Pred. No. 6.1e-145;
  Matches 608; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Qy 354 CCGGTTTGATCCGGTCCCTCGAGTACCAACACCCCTCTTTTTCACCTTCACCTTCATGA 413
Db 2 CCGGTTTGATCCGGTCTTCTCAACACCGGACCCACCTCTCTCACATCAACCCCTCATGA 61

Qy 414 CTTGTACCTTCTTCGAGTACAGCTTTAGCCACCGGAGATGTTCCCGATCTCTCGG 473
Db 62 CCTCGTACCTTCTTCGAGTACAGCTTTAGGAGACGGTGAATGTTCTGATCTCTCGG 121

Qy 474 TCTAGCCAGTCGAAAGACGTTTCGCAACCCACTTACCGTTCCGTTCCCTAAAGGAACGAT 533
Db 122 TTTAGCCAGTCGAAAGACATTCGCAACCCACGTCCTTTCGGTTCCCTCAAGGACTCCAT 181

Qy 534 CGAAGAACCCGGTGTGAAGTCTGTAATGTCGCGGAACCCGTTTGACACATCATCTC 593
Db 182 CGAAGAACCCAGGCGTGAAGTGTGTACTTTGCCGAAACCCGTTGCACATCATCTC 241

Qy 594 TTCGTGCAATTACACCAACATCAATCCGAGTCTAGTGCAGCCCACTTGTGTAGACCA 653
Db 242 CTCGTGCAATTACATCAACATCAATAGTCGGAGGCACTGAGTCCGTCGTTAGAGA 301

Qy 654 AGCTTTTGATCTGTATTCCCGGGAGTGATCGGGTTTGGCCCGTTTGGGAACACATGTT 713
Db 302 AGGGTTTGTATCTGTACTGCGGAGGGGTGATCGGGTTCGGACCGTTTGGGAACACATGTT 361

Qy 714 GGGATCTGGAGAGAGAGCTTGAAGACACGAGCAAGAGTCTCTTTTAAAGTACGAGGA 773
Db 362 GGGATCTGGAAAGAGAGCTTGAGACACGAGAAAGTCTTGTCTTACGTTACGAGA 421

Qy 774 TCTCAAGACGACATCGAGACCAACTTGAAGAGCTTTCGAACTTTTGAAGCTTCCCTTT 833
Db 422 TCTCAAGACGACATCGAGTCTAATCTTGAAGAGCTTTCGAAAGCTTCTTGGACGTTCCCTTT 481

Qy 834 CACCGAAGAGGAGCAAGAGGAGTGTGAAGGCTATCGCGAGCTGTGTAGTTCGA 893
Db 482 CACCGAAGAGGAGCAAGAGGAGTGTGTGATTCGATTCGATCTGTGAGCTTCGA 541

Qy 894 GAATCTGAAGAGTTGGAGGTGAACAACTCAAGTCAAGTTCGATCAAGAACTTTGAGAAATCG 953
Db 542 GAATCTGAAGAGTTGGAGGTGAACAACTCAAGTCAAGTTCGATCAAGAACTTTGAGAAATAG 601

Qy 954 ATTCTTGTTCGGAAGAGAGTGAAGTGAAGTGTGGTTAACTATTGTCACTTCAAGT 1013
Db 602 GCATCTGTTCAGGAAGAGAGTGAAGTGAAGTGTGGTTAACTATTGTCACTTCAAGT 661

Qy 1014 GGAAGAGTTGTCAAGCTTGTGGATGCAAGTGTAGGTGATCTGGTCTCACTTTCAGGT 1072
Db 562 CGAAGAGTTGTCAAGCTTGTGGATGCAAGTGTAGGTGATCTGGTCTCACTTTCAGGT 720

RESULT 2
BZ062934/c
LOCUS
DEFINITION l1c02b1.1.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
sequence.
ACCESSION BZ062934
VERSION BZ062934.1
KEYWORDS GSS, GI:23673253.
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RESULT 4
LOCUS      AV827990
DEFINITION AV827990 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-22-M04 5',
            mRNA sequence.
ACCESSION  AV827990
VERSION     AV827990.1
KEYWORDS    GI:19870050
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE   1 (bases 1 to 574)
            Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
            Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
            Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
            and Shinozaki, K.
            Large scale analysis of Arabidopsis full-length cDNA (2002b)
            Unpublished (2002)
            Contact: Motoaki Seki
            Plant Functional Genomics Research Group
            RIKEN Genomic Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-4359
            Fax: 81-298-36-9060
            Email: msekiorc.riken.go.jp
            An Arabidopsis full-length cDNA library was constructed essentially
            as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
            and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
            al., submitted for publication) digested with BamHI and SalI. This
            clone is in a modified pBluescript vector. Please visit our web
            site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
            details.
TITLE       Location/Qualifiers
JOURNAL     1. 671
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ORIGIN
Query Match      45.9%; Score 494.6; DB 9; Length 671;
Best Local Similarity 88.4%; Pred. No. 1.9e-131;
Matches 565; Conservative 0; Mismatches 59; Indels 15; Gaps 2;

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45  TCAAGCATGAAGACGATTCATCAATGGCGATCCCAAGTTTCTCCATGTGTCAAGCTCGAG 104
70  CTCCTTAAGGAAGCAAAAATTCGCGAGCTCCGAGCGGAGAAAGATGAAGGCTAAGC 129

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FEATURES

Location/Qualifiers
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 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAF109-22-M04"
 /dev stage="plants at various developmental stages from germination to mature seeds"
 /lab_hosts="DRI0B"
 /clone_lib="RAF109"
 /note="Site 1: BamHI; Site 2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) treatments"

ORIGIN

Query Match 45.1%; Score 486; DB 9; Length 574;
 Best Local Similarity 99.2%; Pred. No. 5.2e-129;
 Matches 508; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 ATGCTACCTCAAGCATGAAGAGCATTCCTCAATGGCGATCCCAAGTTTCTCCATGTCTCAC 60
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 QY 63 ATGCTACCTCAAGCATGAAGAGCATTCCTCAATGGCGATCCCAAGTTTCTCCATGTCTCAC 122
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 QY 61 AAGCTCGAGTCTCTTAAGAAGGCAAACTCGCGAGTCCCGAAAGCCGAAGAAGATGAA 120
 Db |||||
 QY 123 AAGCTCGAGTCTCTTAAGAAGGCAAACTCGCGAGTCCCGAAAGCCGAAGAAGATGAA 182
 Db |||||
 QY 121 GGGTAGCTCGGATTCGAGGATGTTGGATTCTTCTTAAGGAGAGGATCGAGA 180
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 QY 183 GGGTAGCTCGGATTCGAGGATGTTGGATTCTTCTTAAGGAGAGGATCGAGA 242
 Db |||||
 QY 181 ACTCGTTACCTTTACCTATTCCTCAAGGGTTTGTGTCACCAAGCCAAAGAGATTCACGCAATC 240
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 QY 243 ACTCGTTACCTTTACCTATTCCTCAAGGGTTTGTGTCACCAAGCCAAAGAGATTCACGCAATC 302
 Db |||||
 QY 241 ATGCTTTCCAAAACATTTTCCATCTCCTCGAAGAGAGTCTGTTCTCGCCACCATACCT 300
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 Db |||||
 QY 363 AAATCCGGTACAACTGGCTTAAAGCTTTAACTTTTCCATCTCCTTAACCGTCAACCGGTTT 422
 Db |||||
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 Db |||||
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 Db |||||
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 Db |||||
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 QY 543 CCAAGTCAAGAGAGCTTCGCAACCCACTTACCG 574
 Db |||||

RESULT 5

CB260303
 LOCUS 635 bp mRNA linear EST 06-NOV-2003
 DEFINITION 81-E9537-013-002-A22-T7R MP12-ADIS-013 Arabidopsis thaliana cDNA clone MP12p770A22Q 5-PRIME, mRNA sequence.

ACCESSION

CB260303

VERSION

CB260303.1 GI:32885076

KEYWORDS

Est.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 635)
 Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
 Mitchell-Olds,T. and Weishaar,B.

AUTHORS

Large-scale identification and analysis of genome-wide

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
 Genome Res. 13 (6), 1250-1257 (2003)
 22683290
 12799357
 Contact: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
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 Seq primer: T7R; CTAATACGACTCACTATAGGA.

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 T7-SalI-CACGGTCCG-Sprime-cDNA-polyA-CC-NotI-SP6; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection', PI: Bernd Weishaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

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 Best Local Similarity 98.0%; Pred. No. 5.5e-129;
 Matches 492; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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 Db 181 CTTTAAAGTACAGAGATCTCAAAGAGAGATCGAGCCAACTTGAAGAGCTTAGCAAG 240
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936 CAAGAACTTTGAGNAATCGATTCTGTTTCGGAAGGAGGAAGTGAAGTGGGTTAACTA 995
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361 CAAGAACTTTGAGNAATCGATTCTGTTTCGGAAGGAGGAAGTGAAGTGGGTTAACTA 420
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996 TTTGTCACTTCACAACTGGAAGAGTGTGAGCTTGTAGTGATGACAAAGTTAGGTGATC 1055
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421 TTTGTCACTTCACAACTGGAAGAGTGTGAGCTTGTAGTGATGACAAAGTTAGGTGATC 480
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1056 TGGTCTCACTTCAGGTTGAGC 1077
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481 TGGTCTCACTTCAGGTTGAGC 502
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RESULT 6
AV442770
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DEFINITION AV442770 Arabidopsis thaliana above-ground organ two to six-week
old Arabidopsis thaliana cDNA clone AP228c04_r 5', mRNA sequence.
ACCESSION AV442770
VERSION AV442770.1 GI:7613187
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 523)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7 (3), 175-180 (2000)
MEDLINE 20363093
PUBMED 10907847
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

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QY 121 GGGCTAAGCTCGGAGTTCCAGAGATGTTGATTTCTTCTTAAGGAGAGGATGAGA 180
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DB 160 GGGCTAAGCTCGGAGTTCCAGAGATGTTGATTTCTTCTTAAGGAGAGATGAGA 219
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QY 361 GATCCGGTTGGCTCGAGTACCAACCACTCTTTTCACTTCCAACTCATGACCTTTGA 420
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RESULT 7
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old Arabidopsis thaliana cDNA clone AP238a12F 3', mRNA sequence.
ACCESSION AV520946
VERSION AV520946.1 GI:8680473
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 641)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7 (3), 175-180 (2000)
MEDLINE 20363093
PUBMED 10907847
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

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Qy 733 TTGAAGAGACGAGAAAGTCTTCTTTTAAAGTACGAGATCTCAAGAGCATCTCGAG 792

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Qy 793 ACCAACTTGAAGAGCTTGAACATCTCTTAGAGCTTCTTTTCCAGGAAGAGGAA 852

Db 461 ACCAACTTGAAGAGCTTGAACATCTCTTAGAGCTTCTTTTCCAGGAAGAGGAA 402

Qy 853 AAGGAGTGTGAAGGTATCGCGAGCTGTAGCTTCAGATCTGAGAGTGGAG 912

Db 401 AAGGAGTGTGAAGGTATCGCGAGCTGTAGCTTCAGATCTGAGAGTGGAG 342

Qy 913 GTGAACAGTCAACAAAGTCGATCAAGAACTTTGAGAACTCGATCTTTTCCGAAAGGA 972

Db 341 GTGAACAGTCAACAAAGTCGATCAAGAACTTTGAGAACTCGATCTTTTCCGAAAGGA 282

Qy 973 GAAGTGTGATGGGTAACTATTTCTACCTTCAAGTGAAGATTTGAGCCTTA 1032

Db 281 GAAGTGTGATGGGTAACTATTTCTACCTTCAAGTGAAGATTTGAGCCTTA 222

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Db 221 GTGATCAGCAAGTTAGTGGATCTGGTCTCACTTTTCAAGTTGAGC 177

RESULT 8
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LOCUS 77-E011179-013-009-J20-TJR MP12-ADIS-013 Arabidopsis thaliana cDNA
DEFINITION clone MP12p770J209Q 5-PRIME, mRNA sequence.

ACCESSION CB260353.1 GI:32885126
VERSION CB260353.1
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsi.s.

REFERENCE 1 (bases 1 to 585)
AUTHORS Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weisshaar,B.
TITLE Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)

JOURNAL MEDLINE
PUBMED
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.6e-122;
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Db 1 ATCAATCCGAGTCAGTGAGCCAGCTTGTCTAGACCAAGCTTTGTATCTGTATTCGCGG 60

Qy 676 GGAGTGATCGGTTTGGCCCGTTTGGGAACACATGTTGGATCTGGAGAGAGCTTG 735

Db 61 GGAGTGATCGGTTTGGCCCGTTTGGGAACACATGTTGGATCTGGAGAGAGCTTG 120

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Db 121 AAGAGCAGAGAAAGTCTCTTTTAAAGTACGAGATCTCAAGAGCATCTCGAGACC 180

Qy 796 AACTTGAAGAGCTTGCACAACTTCTTAGAGCTTCTTCCAGGAAGAGGAAACGAAAG 855

Db 181 AACTTGAAGAGCTTGCACAACTTCTTAGAGCTTCTTCCAGGAAGAGGAAACGAAAG 240

Qy 856 GGAGTTGTGAAGGTATCGCCAGCTGTAGCTTCGAGATCTCAAGAGTTCGAGGTG 915

Db 241 GGAGTTGTGAAGGTATCGCCAGCTGTAGCTTCGAGATCTCAAGAGTTCGAGGTG 300

Qy 916 AACAACTCAACAAAGTCGATCAAGAACTTTGAGAACTCGATTCGTTTGGAAAGGAGAA 975

Db 301 AACAACTCAACAAAGTCGATCAAGAACTTTGAGAACTCGATTCGTTTGGAAAGGAGAA 360

Qy 976 GTGAGTGTGGTTAACTATTGTGACCTTCAAGTGAAGATTTGAGCCTTAGTG 1035

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DEFINITION old Arabidopsis thaliana cDNA clone AP228c04_3', mRNA sequence.
ACCESSION AV441110
VERSION AV441110.1 GI:7611490
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 638)
REFERENCE
AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
JOURNAL DNA Res. 7 (3), 175-180 (2000)
MEDLINE 20363093
PUBMED 10907847
COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
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 Best Local Similarity 100.0%; Pred. No. 4.8e-122;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 616 ATCAAAATCCGAGTCAGTGAGCCAGCTCTTGCTAGACCAAGCTTTGATCTGTATTGCCGG 675
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 DB 578 GGAGTGATCGGGTTGGCCCGTTTGGGAACACATGTTGGTACTCTGGAGAGAGAGCTTG 519
 QY 736 AAGAGACACGAGAAAGTCTTTTAAAGTACGAGATCTCAAAGACGATCGAGACC 795
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 DB 458 AACTTGAAGAGGCTTCAACTTTCTTAGAGCTTCTTACCAGGAAGGAGGACGAAAG 399
 QY 856 GGAGTTGTGAAGGCTATCGCGAGCTGTAGCTTCGAGAAATCTGAAGAAAGTTGGAGGTG 915
 DB 398 GGAGTTGTGAAGGCTATCGCGAGCTGTAGCTTCGAGAAATCTGAAGAAAGTTGGAGGTG 339
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 QY 976 GTGAGTGATGGGTAACTATTCTGACCTTCAAGTGGAAAGATTGTGAGCTTAGTG 1035
 DB 278 GTGAGTGATGGGTAACTATTCTGACCTTCAAGTGGAAAGATTGTGAGCTTAGTG 219
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 DB 218 GATGACAAAGTGTGATCGGTCTCACTTTCAAGTTGAGC 177
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 LOCUS 727 bp mRNA linear EST 10-JUL-2003
 DEFINITION BN45.052G01F020104 BN45 Brassica napus cdna clone BN45052G01, mRNA sequence.
 ACCESSION CD837475
 VERSION CD837475.1 GI:32519415

KEYWORDS
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics Unpublished (2003)
JOURNAL Contact: Genoplante
COMMENT Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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 Best Local Similarity 82.2%; Pred. No. 1.4e-119;
 Matches 564; Conservative 0; Mismatches 104; Indels 18; Gaps 3;
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 DB 111 CACAGCAGAGCTCTCTCAAGGAAGAGCAAAAGCCGAGACCCGAGCGCCAGAGAA 170
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 QY 412 GACCTTGATACCTTTCTTCGAGTACAAGCTTTACGCAACGAGAGATGTTCCCGATCTTCG 471
 DB 462 GACCTCGTACCTTTCTTCGAGTACAAGCTTTACGCAACGAGAGATGTTCTGATCTCTCC 521
 QY 472 GGTCTAGCCAGTCCAAAGACGTTCCCAACCCCACTTACCGTTTCGGTTCCCTAAGGAAACG 531
 DB 522 GGTCTAGCTAGTCCAAAGAACATTCGCAACACACGTCCTTTTCGGTTCTCTCAAGGGCTCC 581
 QY 532 ATCGAGAAACCCGGTGTGAAGTCTGTGACTTGTCCCGGAAACCCGTTTGACATTCATC 591
 DB 582 ATCGAGAAACCCGGGAGCGAAGGTTGTGACTTGTGTGCGAAACCCGTTTGCACACGTTTCATC 641

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QY 285 TCTCGCCACCATCACTTAATCCGGTACAACTGGCTAAAAGCTTTAACTTTACCATCTT 344
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QY 345 TAACCGTCAACCGGTTTATCGGTTGCTCC---TGAAGTACCAACCAACCCCTCTTTTCACTTC 401
Db 181 TACCGTCACTCGGTTTATCGGTTTCTCTCATCAAGTTCGACCAACCCCTCTTCTCACATC 240
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Db 481 CTTGCTAGACCAAGCTTTTATCTGATCTGATTCGCGGGAGT 519

RESULT 13
CD833738
LOCUS
DEFINITION
CD833738 651 bp mRNA linear EST 10-JUL-2003
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 651)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).

FEATURES
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/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Query Match 37.2%; Score 400.2; DB 14; Length 651;
Best Local Similarity 82.5%; Pred. No. 3 6e-104;
Matches 501; Conservative 0; Mismatches 88; Indels 18; Gaps 3;

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Db 645 TCTTCGT 651

RESULT 14
CD822905
LOCUS
DEFINITION
CD822905 657 bp mRNA linear EST 10-JUL-2003
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 657)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).

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/clone="BN25047A10"
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/clone_lib="BN25"

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Query Match 34.1%; Score 367.2; DB 14; Length 657;
Best Local Similarity 80.8%; Pred. No. 1.3e-94;
Matches 496; Conservative 0; Mismatches 98; Indels 20; Gaps 5;
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DB 51 ATGGCGACCTCAAGCATCAAGAGTGTTCCTCAATATATGGCATCCCAAGTTTATCCATTGC 110
QY 58 CACAGCTCGAGCTCCCTTAAGAGGCAAACTCGCGACGTCCCGA-----AAGCGGA 111
DB 111 CACAAGCACGAGCTCCCTCAAGGAAGAAGCAAGCCGAGACCCGAGCCCAAGAGAA 170
QY 112 GAAGATGAAGGCTTAAGTGGAGTGTCCAGAGATGTGGATTCTCTTCTTAAGGAGAGA 171
DB 171 GAAGAGAGGCTTAAGTACGAGTCTTAGAGATGTGGACTCTCTCTTAAGGAGAGA 230
QY 172 GGATGGAGAACTCGTTACCTTACTATTCAAGGTTTGGTCCCAAGCAAGAGATT 231
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QY 232 CAAGCCATCATGTCTTCCAAAAACATTTCCAAATCCCTCGAAAAACGACGTCTCTCGCC 291
DB 291 CATGCCATCATGTCTTCCGAAACATTTCAAGCCTCTTCCAAAGATGTTATCTTGCT 350
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DB 351 ACCATACCAAAATCCGGTACAACTGTTTAAAGCTTAAACATTTACCTCTCTTAACCGA 410
QY 352 CACCGTTGTATCCGGTTGCGCTCGAGTACCAACCAACCTCTTTTCACTTCCAACTCAT 411
DB 411 CACCGTTGTATCCGGT-----TCTGACCACTCTCTCTCATCAATCAACCTCAT 461
QY 412 GACCTTG-TACCTTCTTCGAGTACAAGCTTTACGCCAAGGAGATTTCCGATCTCTC 470
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QY 471 GGGTCTAGCAGTCCAGAGGTTTCGCAACCCACTTACCTGCTCGTTCCCTTAAGGAAC 530
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QY 531 GATCGAGAAACCCGG-TGTGAAGTCTGTACTTGTGCGGAAACCCGTTTGACACATTC 589
DB 582 AATCGAGAACCGGACCTGAAGCTGTGACTTGTGCGGAAACCCGTCGACCCGTTCA 641
QY 590 TCTCTCTGTCAT 603
DB 642 TCTCTCTGTCAT 655

RESULT 15
LOCUS CC952179/c 760 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIGS48TF BO.1.4.1.6_KB_nuc Brassica oleracea genomic clone
BOIGS48, genomic survey sequence.

CC952179
VERSION CC952179.1 GI:33790676
KEYWORDS GSS

SOURCE Brassica oleracea
ORGANISM Brassica oleracea

REFERENCE 1 (bases 1 to 760)
AUTHORS Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIGS48TR
Contact: Chris Town

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
Location/Qualifiers
source
1..760

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/db_xref="taxon:3712"
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/clone_lib="BO.1.4.1.6_KB_nuc"
/note="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN

Query Match 34.0%; Score 365.8; DB 29; Length 760;
Best Local Similarity 81.0%; Pred. No. 3.4e-94;
Matches 469; Conservative 0; Mismatches 92; Indels 18; Gaps 3;
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DB 570 ATGGCGACCTCAAGCATCAAGAGTGTTCCTCAATATATGGCATCCCAAGTTTATCCATTGC 511
QY 58 CACAAGCTCGAGCTCTTAAAGAGGCAAACTCGCGACGTCCCGA-----AAGCCGAA 111
DB 510 CACAAGCACGAGCTCTCTCAAGAGAGGCAAAAGCCGAGACCCGAGCCCAAGAGAA 451
QY 112 GAAGATGAAGGCTTAAGTGGAGTTCGAGTTCGAGATGTGGATTCTCTTCTTAAGGAGAGA 171
DB 450 GAAGAAGAAGGCTTAAGCTAGAGTCTTAGAGATGTGGACTCTCTTCTTAAGGAGAGA 391
QY 172 GATCGGAGACTCGTTACTTTTACCTATTCGAGGTTTTCGTCGCAAGCAAGAGATT 231
DB 390 GGTGGAGAACTCGTCATCTTTACCTGTTCCAGGCTTTTGTGTCGCAAGCCAGAGATT 331
QY 232 CAAGCCATCATGTCTTTTCCAAAAACATTTCCAATCCCTCGAAAAACGAGCTGTTCTCGCC 291
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QY 352 CACCGTTGTATCCGGTTGCGTTCGAGTACCAACCACTCTTTTCACTTCCAAACCTCAT 411
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QY 412 GACCTTGATCCTTTCTTCGAGTACAAGCTTTACGCCAAGGAGATGTTCCGATCTCTCG 471
DB 159 GACCTCGTACCTTTCTTCGAGTACAAGCTTTACGCCAAGGAGATGTTCTGATCTCTCC 100
QY 472 GGTCTAGCCAGTCCCAAGACGTTCCCAACCCACTTACCGTTTCGGTTCCCTTAAAGAAACG 531
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QY 532 ATCGAGAAACCCGGTGTGAAGTCTGTGATCTGTGTCGG 570
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Job time : 3232 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2004, 02:51:44 ; Search time 97 Seconds
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Title: US-10-019-931-1

Perfect score: 1077

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	47.6	4.4	7218	1	US-08-232-463-14
3	35.8	3.3	1236	2	US-08-741-134-5
4	34.2	3.2	474	4	US-09-621-976-18033
5	33.8	3.1	474	4	US-09-621-976-18033
6	33.8	3.1	12720	1	US-08-403-866-11
7	33.2	3.1	832	4	US-09-621-976-2813
8	32.4	3.0	3910	4	US-09-302-6208-91
9	32.4	3.0	3910	4	US-09-912-161-14
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11	31.6	2.9	11303	4	US-08-961-527-115
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14	31.4	2.9	6794	4	US-09-491-356C-2
15	31.2	2.9	828	4	US-09-107-532A-359
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17	31.2	2.9	9636	1	US-08-323-170B-1
18	31.2	2.9	9636	1	US-08-954-441-1
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20	31.2	2.9	4403765	3	US-09-103-840A-2
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22	31	2.9	505	4	US-09-621-976-15639
23	30.8	2.9	3826	4	US-09-302-6208-90
24	30.8	2.9	3826	4	US-09-912-161-13
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26	30.6	2.8	2025	4	US-09-620-312D-834
27	30.6	2.8	5304	4	US-09-023-655-664

Query Match

4.5%; Score 48; DB 1; Length 7218;

ALIGNMENTS

RESULT 1

US-08-232-463-14

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 30472/114 IMMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7218 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: pTZ9pt-F18

US-08-232-463-14

Sequence 296, App
Sequence 4884, Ap
Sequence 8976, Ap
Sequence 292, App
Sequence 4830, Ap
Sequence 294, App
Sequence 4859, Ap
Sequence 280, App
Sequence 4842, Ap
Sequence 272, App
Sequence 4897, Ap
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 984, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 327, App

Best Local Similarity 5.8%; Pred. No. 1.2e-05;
Matches 24; Conservative 216; Mismatches 176; Indels 0; Gaps 0;
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Db 1035 GAGCTTGCTGCGAGTCCAGGAGCTTCCGATTTTTTTTTTTTTTTTTT 1094
QY 265 TCCCTGAAACGAGCTGCTTCGCGACCATACCTAAATCCGCTCAACCTGGCTAAA 324
Db 1095 YY 1154
QY 325 GCTTTAACTTTCACATCTTAACCGTCACCGTTTTCGCGTTCGCTCGAGTCAAC 384
Db 1155 YY 1214
QY 385 CACCTCTTTCACCTTCGACCTTCGAGTTCGAGTTCGAGTTCGAGTTCAC 444
Db 1215 YY 1274
QY 445 GCCAACGAGATGTCGCGATCTCTCGGCTAGCCAGTCCAGAACTTCGCAACCCAC 504
Db 1275 YY 1334
QY 505 TTACGCTGCTTCCCTAAAGAAACGATCGAGAACCCGCTGGAAGTCTGCTACTTG 564
Db 1335 YY 1394
QY 565 TGCGGAACCGTTTGACATTCATCTCTCGGCTACACCAACCAACATCAA 620
Db 1395 YY 1450

RESULT 2

US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Hardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-F1s
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Query Match 4.4%; Score 47.6; DB 1; Length 7218;
Best Local Similarity 5.0%; Pred. No. 1.6e-05;
Matches 20; Conservative 214; Mismatches 168; Indels 0; Gaps 0;
QY 674 GGGAGTGTGCGGTTTGGCCGTTTGGGAACACATCTTGGTACTGGAGAGAGCT 733
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Db 1369 RR 1310
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Db 1129 RR 1070
QY 1034 TGGATGCAAGTTAGTGTGATCTGCTCTCACTTCAGGTTGA 1075
Db 1069 RRRATCGCAAGCTCCTCGACTGCGAGCCAGCTCGGAATTA 1028

RESULT 3

US-08-741-134-5
; Sequence 5, Application US/08741134
; Patent No. 5861498
; GENERAL INFORMATION:
; APPLICANT: Litwack, Gerald
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; TITLE OF INVENTION: IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING
; TITLE OF INVENTION: AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5861498ris
; STREET: One Liberty Place - 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.11
; SOFTWARE: Wordperfect for Windows 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,134
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,163
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 424

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; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-2090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1236 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1236
; US-08-741-134-5

Query Match      3.3%; Score 35.8; DB 2; Length 1236;
Best Local Similarity 51.6%; Pred. No. 0.07; 77; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 77;

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DB 525 AGACGAAGATGAGAGCGTGACATCTATGACAGTGAAGACTACGACTTGACCCAGATGA 584
QY 851 GAAGGGAGTTGTAAGGCTATCCCGAGCTGTGCTAGCTTCGGAATCTGAAGAAGTTGG 910
DB 585 GGATGAATATTGGCGACGACATGGACGACTTGATGACGAAGAGGAAGAAGTTCG 644
QY 911 AGGTGAACAAGTCAACAAGTCGATCAAGAACTTTGAGA 949
DB 645 TATTGAAGAAGTCCAAGAAGAAGATGAAGAAGATAATGA 683

RESULT 4
US-09-621-976-18033
; Sequence 18033, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18033
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 16
; OTHER INFORMATION: n=a, g, c or t
; US-09-621-976-18033

Query Match      3.1%; Score 33.8; DB 4; Length 474;
Best Local Similarity 14.0%; Pred. No. 0.18;
Matches 42; Conservative 131; Mismatches 123; Indels 3; Gaps 1;

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DB 320 MYRRGGKYRRARRWTWARRRMTWTWYKWKSCWKKWKKRKYMKCYWWR 261
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DB 260 KYCCMRKKRRRGGKRRRSYKSGSYTYKGGKGGTGKGGKAMSKGRRRAMTTT 201
QY 713 TGGGATCTGGAGAGAGAGCTTGAAGAGACACAGAAAGTCTTCTTTTAAGGTACGAG 772
DB 200 YYYKKKW---RSYWAARGKTTKKWAMMMWMMWYMRSMYMYKKWAAAKWSCCMARK 144
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DB 143 KGSSSGRWYMWKRGCTCMGRRRWYRMRMCWYCTKGSMAWMSGKRAAMCCCKYY 84
QY 833 TCACCGAAGAGAGAGGAAGAGGGAGTTGTGAAGGCTATCGCCGAGCTGTGTAGCTTC 891
DB 83 TWMCMAAAAMWMTWAAAAAAMMRSCGRMSKKKGGKSGVRSSSCYKSMRKYCCMRSYWM 25

RESULT 6
US-08-403-866-11
; Sequence 11, Application US/08403866
; Patent No. 5643779
; GENERAL INFORMATION:
; APPLICANT: Ehrlich, Stanislaw
; APPLICANT: Godon, Jean-Jacques
; APPLICANT: Renault, Pierre
; TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
; TITLE OF INVENTION: synthase from Lactococcus and its applications
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICANT NUMBER: US/08/403,866
; FILING DATE:
; CLASSIFICATION: 435
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DB 371 GWTAAWACTKTCGTGAAAATGTCTCATGTCTGTAAATCCAGCA 415

RESULT 5
US-09-621-976-18033/c
; Sequence 18033, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18033
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 16
; OTHER INFORMATION: n=a, g, c or t
; US-09-621-976-18033

Query Match      3.1%; Score 33.8; DB 4; Length 474;
Best Local Similarity 14.0%; Pred. No. 0.18;
Matches 42; Conservative 131; Mismatches 123; Indels 3; Gaps 1;

QY 593 CTTCTGGCATTACACCAACATCAATCCGAGTCAGTGAGCCAGCTTCTGTAGACC 652
DB 320 MYRRGGKYRRARRWTWARRRMTWTWYKWKSCWKKWKKRKYMKCYWWR 261
QY 653 AAGCTTTTGAATCTGATTGCCGGGAGTCAATCGGTTTGGCCGTTTGGGAACACATGT 712
DB 260 KYCCMRKKRRRGGKRRRSYKSGSYTYKGGKGGTGKGGKAMSKGRRRAMTTT 201
QY 713 TGGGATCTGGAGAGAGAGCTTGAAGAGACACAGAAAGTCTTCTTTTAAGGTACGAG 772
DB 200 YYYKKKW---RSYWAARGKTTKKWAMMMWMMWYMRSMYMYKKWAAAKWSCCMARK 144
QY 773 ATCTCAAAGACGACATCGAGACCAACTTGAAGAGGCTTGCACACTTCTTAGAGCTTCTT 832
DB 143 KGSSSGRWYMWKRGCTCMGRRRWYRMRMCWYCTKGSMAWMSGKRAAMCCCKYY 84
QY 833 TCACCGAAGAGAGAGGAAGAGGGAGTTGTGAAGGCTATCGCCGAGCTGTGTAGCTTC 891
DB 83 TWMCMAAAAMWMTWAAAAAAMMRSCGRMSKKKGGKSGVRSSSCYKSMRKYCCMRSYWM 25

RESULT 6
US-08-403-866-11
; Sequence 11, Application US/08403866
; Patent No. 5643779
; GENERAL INFORMATION:
; APPLICANT: Ehrlich, Stanislaw
; APPLICANT: Godon, Jean-Jacques
; APPLICANT: Renault, Pierre
; TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
; TITLE OF INVENTION: synthase from Lactococcus and its applications
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICANT NUMBER: US/08/403,866
; FILING DATE:
; CLASSIFICATION: 435
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; GENERAL INFORMATION:
; APPLICANT: David, Craft L.
; APPLICANT: Madduri, Krishna
; APPLICANT: Loper, John C.
; TITLE OF INVENTION: CYTOCHRO

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; TITLE OF INVENTION: THERETO
; FILE REFERENCE: M6368 (1010-35)
; CURRENT APPLICATION NUMBER: US/09/912,161
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 3910
; TYPE: DNA
; ORGANISM: Candida tropicalis
US-09-912-161-14

Query Match      3.0%; Score 32.4; DB 4; Length 3910;
Best Local Similarity 54.1%; Pred. No. 2.6;
Matches 66; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 883 TGTAGCTTCGAGATCGTGGAGTGGAGTCAACAGTCAACAGTCAAGTCAAGAAC 942
Db 3718 TGGCGCTCTGTGTGCAAGAAGTCTGTCATGAATCTGTTGAAGATGTCGATCTCG 3659

QY 943 TTTGAGATCGATTTCTTTTCGAAAGAGAGTGAAGTGAATGGTTAACTATTGTCA 1002
Db 3658 TCCAAGTGTGCTGTGTTGTTCTGGAAGCCCAAGTTGATCAAGCCCGTGGTCAACTTCTCA 3599

QY 1003 CC 1004
Db 3598 CC 3597

RESULT 10
US-09-313-294A-6743/C
; Sequence 6743, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura V.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6743
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700352328H1
US-09-313-294A-6743

Query Match      3.0%; Score 32.2; DB 4; Length 285;
Best Local Similarity 57.4%; Pred. No. 0.46;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 574 CCGTTTCACATTCATCTCTGTGGCATTACACCAACATCAATCCGAGTCAGTG 633
Db 109 CCGTTTGACATCCCATCAACAGGAGGATCGATCGCAGCAATCCAAAGTTT 50

QY 634 AGCCAGTCTGTGTCAGACCAAGCTTTTGTATGTCGTCGCG 674
Db 49 AGCAATCTGTGTAAGCATATCTTTTATGTATGATCTTCTG 9

RESULT 11
US-08-961-527-115/c
; Sequence 115, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
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```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: P3340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-115

Query Match      2.9%; Score 31.6; DB 4; Length 11303;
Best Local Similarity 54.2%; Pred. No. 11;
Matches 64; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 883 TGTASCTTCGAGATCTGAAGAGTGGAGTGAACAGTCAACAGTCAAGTCAAGAAC 942
Db 8207 TGTACTTTAAGCAATTTGAAGAGGCTGTTCTTAAAGCAGGAAACCACTTGACAAATAC 8148

QY 943 TTTGAGATCGATTTCTTTTCGAAAGAGAGTGAAGTGAATGGTTAACTATTGT 1000
Db 8147 CTCCTCAAGCCTATATTCCTATTCATCCATGGGAATTGAAATGCTAATTTGATTCT 8090

RESULT 12
US-09-013-067A-7
; Sequence 7, Application US/09013067A
; Patent No. 6057144
; GENERAL INFORMATION:
; APPLICANT: TOKOYASU, KEN
; APPLICANT: MORI, YUTAKA
; APPLICANT: HAMATSU, SHIOKA
; APPLICANT: HAYASHI, KIYOSHI
; TITLE OF INVENTION: CHITIN DEACETYLASE GENE, VECTOR CONTAINING
; TITLE OF INVENTION: SAID GENE AND TRASFORMANT
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/013,067A
; FILING DATE: 01-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 9-345737
; FILING DATE: 02-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 8361-0002-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PCR REACTION PRODUCTS"
; ORIGINAL SOURCE:
; ORGANISM: Colletotrichum lindemuthianum
; STRAIN: ATCC 56676
; US-09-013-067A-7

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Best Local Similarity 54.9%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 51;

QY 338 CCATCCTTAACCGTCACCGGTTTGATCGGTTGCTCGAGTACCAACCCCTTTTCA 397
Db 107 CCATCCTCAAGTCACCGCCGCTGGTGGTGTCTGACTACGACGACGGTCTTTCA 166

QY 398 CTTCCACCCCTCATGACCTTGACTTCTTCGAGTACAAGCTTACGCCAAC 450
Db 167 CTTTACCGCTCAGCTCCTCGACATCTTGAAGCAGAACGACGTCAGGCGACC 219

RESULT 13
US-09-489-847-44
; Sequence 44, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 2572
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (2527)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-489-847-44

APPLICATION NUMBER: US/09/013,067A
FILING DATE: 01-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-345737
FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 8361-0002-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PCR REACTION PRODUCTS"
ORIGINAL SOURCE:
ORGANISM: Colletotrichum lindemuthianum
STRAIN: ATCC 56676
US-09-013-067A-7

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Best Local Similarity 53.7%; Pred. No. 4.3; Indels 0; Gaps 0;
Matches 65; Conservative 0; Mismatches 56;

QY 863 TGAAGGCTATCGCCGAGCTGTGTAGCTTCGAGAATCTCGAAGAAGTTGAGGTGAACAACT 922
Db 854 TGGTCGCCATCGCTCGGTGCTATGCTTACCGGAAGCAGAAAAAGAGATGAGGAATGAGT 913

QY 923 CAACAAGTCGATCAAGAACITTTGAGAATCGATTCTTTTCGGAAGAGAAAGTGAAGT 982
Db 914 CGGCCACGAGGGGGAAGACTTCCCATGACAGACATCGCTCCGACAGAGAGGTGACAG 973

QY 983 A 983
Db 974 A 974

RESULT 14
US-09-491-356C-2
; Sequence 2, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ1.3
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6794
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-491-356C-2

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Best Local Similarity 48.6%; Pred. No. 8.8; Indels 0; Gaps 0;
Matches 86; Conservative 0; Mismatches 91;

QY 777 CAAGACGACATCGAGACCAACTTGAAGAGGCTTGCACATTTCTTAGAGCTTCCTTTTCA 836
Db 4722 CACTGTCGACATGCAGTCCAACTGCTTCACTACTGTGTGGACATGCTGAGCGT 4781

QY 837 CGAAGAAGAGGAAAGGAGGAGTTGTGAAGGCTATCCCGAGCTGTGTAGCTTCGAGAA 896
Db 4782 GCTCATCAATGGGACATTGGCTGCAGACATGCTAGCATCTCGCAAGTAGCATGGAGGA 4841

QY 897 TCTGAAGAAGTTGGAGGTGAACAAGTCAACAAGTCGATCAAGAACTTTGAGAATCG 953
Db 4842 AAACAAGCGTGCATACATGAACCTGGCGAAGAGTTGCAGAAGGAGTTGGGGGAGCG 4898

RESULT 15
US-09-107-532A-359
; Sequence 359, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Maximum Match 100%

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- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	355.4	33.0	1311	13	US-10-424-599-58871 Sequence 58871, A
2	229.2	21.3	981	9	US-09-938-842A-2049 Sequence 2049, Ap
3	229.2	21.3	981	11	US-09-938-842A-2049 Sequence 2049, Ap
4	221.8	20.6	787	13	US-10-424-599-82242 Sequence 82242, A
5	219.2	20.4	996	9	US-09-938-842A-1027 Sequence 1027, Ap
6	219.2	20.4	996	11	US-09-938-842A-1027 Sequence 1027, Ap
7	200.8	18.6	1041	17	US-10-437-963-55857 Sequence 55857, A
8	184.2	17.1	271990	15	US-10-195-144-87 Sequence 87, Appl
9	184.2	17.1	271990	16	US-10-345-072-87 Sequence 87, Appl
10	166	15.4	2067	15	US-10-195-144-80 Sequence 80, Appl
11	166	15.4	2067	16	US-10-345-072-80 Sequence 80, Appl
12	161.8	15.0	1077	17	US-10-437-963-55524 Sequence 55524, A
13	157	14.6	654	17	US-10-021-323-11330 Sequence 11330, A
14	155	14.4	1068	17	US-10-437-963-94656 Sequence 94656, A

15	147.4	13.7	1041	15	US-10-259-165-331	Sequence 331, App
16	147.4	13.7	1041	17	US-10-437-963-68828	Sequence 68828, A
17	141.8	13.2	1017	16	US-10-259-194A-3	Sequence 3, Appl
18	141.8	13.2	1017	17	US-10-437-963-27879	Sequence 27879, A
19	138.2	12.6	610	17	US-10-021-323-11419	Sequence 11419, A
20	135.8	12.6	1403	13	US-10-425-114-21478	Sequence 21478, A
21	135.8	12.6	1526	13	US-10-425-114-27795	Sequence 27795, A
22	131.8	12.2	1011	17	US-10-437-963-96500	Sequence 96500, A
23	131.2	12.2	1056	17	US-10-437-963-51349	Sequence 51349, A
24	126	11.7	984	15	US-10-259-165-443	Sequence 443, App
25	126	11.7	987	15	US-10-259-165-113	Sequence 113, App
26	125.8	11.7	1050	16	US-10-259-194A-15	Sequence 15, Appl
27	125.8	11.7	1050	17	US-10-437-963-54999	Sequence 54999, A
28	121.8	11.3	1021	17	US-10-437-963-73855	Sequence 73855, A
29	118.6	11.0	1047	17	US-10-437-963-50078	Sequence 50078, A
30	117	10.9	1047	16	US-10-259-194A-379	Sequence 379, App
31	112.8	10.5	1461	16	US-10-260-238-1003	Sequence 1003, App
32	112.8	10.5	1461	16	US-10-260-238-1003	Sequence 1003, App
33	110.6	10.3	1482	17	US-10-437-963-75177	Sequence 75177, A
34	108.6	10.1	1032	16	US-10-259-194A-329	Sequence 329, App
35	108.6	10.1	1355	17	US-10-437-963-56891	Sequence 56891, A
36	108.4	10.1	1033	17	US-10-437-963-72606	Sequence 72606, A
37	107.6	10.0	2496	17	US-10-437-963-76496	Sequence 76496, A
38	106.8	9.9	1878	17	US-10-437-963-72617	Sequence 72617, A
39	100.8	9.4	528	17	US-10-021-323-14619	Sequence 14619, A
40	100.8	9.4	1192	9	US-09-854-122-15	Sequence 15, Appl
41	98	9.1	1462	16	US-10-259-194A-643	Sequence 643, App
42	97.4	9.0	512	17	US-10-437-963-55626	Sequence 55626, A
43	88.8	8.2	1269	17	US-10-437-963-31735	Sequence 31735, A
44	88.6	8.2	629	17	US-10-437-963-56759	Sequence 56759, A
45	88.6	8.2	948	17	US-10-437-963-49745	Sequence 49745, A

ALIGNMENTS

RESULT 1

US-10-424-599-58871
; Sequence 58871, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(33223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 58871
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1311)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_24172C.1
US-10-424-599-58871

Query Match 33.0%; Score 355.4; DB 13; Length 1311;
Best Local Similarity 61.4%; Pred. No. 1.3e-107;
Matches 591; Conservative 0; Mismatches 366; Indels 6; Gaps 1;
QY 111 AGAAGATGAGGGCTAAGCTCGAGTTCACAGATGTGGATTCCTCTTAAGGAG 170
Db 107 AGAAGATGAGGGCTAAGCTCGAGTTCACAGATGTGGATTCCTCTTAAGGAG 166
QY 171 AGGATGGAGAACTCGTTACCTTACTTCCAAAGGTTTGGTGCCAAAGCAAGAT 230

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Db 167 AGTTTGGAGAACAGTTATATATATCTATTTCAAGGATTTTGTGCGAGCCATTGGAAT 226
Qy 231 TCAGCCATCATGCTTTTCCAAAACATTTCCATCCCTCGAAACGACGCTGTTCTCGC 290
Db 227 CCAAGCAATATCACTTTTCAAGAGCACTTCCAGACTTAAGACAGTATGTTATTTGGC 286
Qy 291 CACCATACCTAAATCCGGTCAACCTGGCTAAAGCTTTAACTTTTCACTCCATCCCTTAACCG 350
Db 287 CACAATTCAAAATCAGTACCACTTGGCTGAAAGCTCTCACCTTTTGGCAATTTGCAATCG 346
Qy 351 TCACGGTTTTCATCCGGTTCCTCGAGTACCAACACCTCTTTTCACTTCCACCTCA 410
Db 347 CCATCTCATAGTATCACTACATCAATGTCTACATCTTTGTTTACTTCTATCTCTCA 406
Qy 411 TGACCTTGTACCTTTTTCGAGTACAAGCTTTTACGCCAACG-----GAGATGTTCCCGA 464
Db 407 TGAATCTGTGCTTTTATAGAAATACACCGTTTATGGTAATGCCCTAGCCATGTTCCAAA 466
Qy 465 TCTCTGGGTTCAGCAGTCAAGAACGTTCCGAACCCACTTACCGTTCGGTTCCTTAA 524
Db 467 CCTATCCAAATGACTGAGCCAAAGACTTTTGGTACACATATTCATTCATGCAITGGC 526
Qy 525 GMAACGATCGAGAAACCCGGTGTGAAGTCTGTACTTGTGCGCGAACCCGTTTTCACAC 584
Db 527 CAAGTCCATCAAGGAGTCCATAGTAGAATAATTTATATATGTAGGAACCCACTTGACAC 586
Qy 585 ATTCAATCTCTCGTGGCATTACACCAACATCAATCCAGTCACTGAGCCAGCTT 644
Db 587 TTTTGTGTCTATTGGATTTTCTCAACAAATTAAGCCAGAACATTTACTGAAATTTGA 646
Qy 645 GCTAGACCAAGCTTTTGTATGTTGCGGGAGTGTATGGTTCGGCGGTTTTCGGGA 704
Db 647 ACTAGGGAAGCTTTTGAAGTATGCAAGAGATATAGGGTTTGGTCCAACTTGGGA 706
Qy 705 ACACATGTTGGGATACTCGAGAGAGAGCTTGAAGAGACCAAGAGAAAGTCTTTTAAAG 764
Db 707 CCAATGTTGGTTATTGGAAGGAGATATAGTAGGCTAGTAAGGTTTGTCTTTGAA 766
Qy 765 GTACGAGATCTCAAGACGACATCGACACCACTTGAAGAGGCTTGCACCTTTCTTGA 824
Db 767 GTACGAGATCTTAAAGAGATGCAATTTTCATGTGAAGAAATAGCGAGTCTTAGG 826
Qy 825 GCTTCTTTCACCGAAGAGAGAACGAAAGGAGTTGTGAAGCTATCGCCGAGCTGTG 884
Db 827 ATGTCCTTTCATTCGGAGGAGAGAGTGTAGGGACTATTGAGAGCAATATCAAGCTATG 886
Qy 885 TAGCTTCAGAAATCTGAAGAGTTGGAGGTGAACAAGTCAACAAGTCGATCAAGAACTT 944
Db 887 CAGCTTCGAGAAGTGAAGGAATTTGGAGGCAATTAATCTCGAACTTTGCTAGGAACCT 946
Qy 945 TGAGATCGATCTTTGTTTTCGAAAGGAGAGTGAAGTATGAGTGGTAACTATTGTCACC 1004
Db 947 TGAGAAAGTACTTTTCCGAAGGCTGAATGGAGATTGGTGAATCTTACCTTTCCCC 1006
Qy 1005 TTCACAGTGAAGATTTGTCAGCTTGTAGTGATGAACAAGTGAAGTGTGCTCTCAC 1064
Db 1007 TGAATGGGTGAAGATTTATCGCAATTTATGGAAGAAAGTAAAGTGGGTGAGCTTGTG 1066
Qy 1065 TTT 1067
Db 1067 ATT 1069

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RESULT 2

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US-09-938-842A-2049
; Sequence 2049, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

```

```

; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2049
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-2049

Query Match 21.3%; Score 229.2; DB 9; Length 981;
Best Local Similarity 54.9%; Pred. No. 2.3e-65;
Matches 525; Conservative 0; Mismatches 413; Indels 18; Gaps 3;

Qy 112 GAAGATGAAGGGCTAAGCTGCGAGTTCGAAGAGATGTTGGATCTCTTCTTCTTAAGAGAGA 171
Db 34 GGAGATGAAGATCTGACACAGAAACAAGAGCTCTGTATCTCTTCTTCTTCTTAAGAGAGA 93
Qy 172 GGATGGAGAACTCGTTTACCTTTTACCTATTCCAAAGGGTTTGGTGCCAAAGCCAAAGAGATT 231
Db 94 GGTGGTAGTGAAGTAAATATATGAATTCGAAGACTTGGCACACACAAGCTATTTTA 153
Qy 232 CAAGCCATCATGCTTTTCCAAAACATTTCCAAATCCCTCGAAACGAGAGTGTCTCTGCC 291
Db 154 CAAGGAATCTTATCTGTCGCAAAACGCTTTGAAGCTAAAGATTCGACATATCTCTGTC 213
Qy 292 ACCATACCTAAATCCGGTACACCTGGCTAAAGCTTTAACTTTTCAACCATCTTAAACCGT 351
Db 214 ACTAATCTTAATCAGGTACCACTTGGTTAAAGCTCTTGCTTTGCTCTCTCTTAACCGA 273
Qy 352 CACCGGTTTGTATCCGGTTGCTCTCGAGTACCAACCACTCTTTTCACTTCCAAACCTCAT 411
Db 274 CACAAGTT---TCCAGTTTCTTCTTCTGTAACCATCTCTTCTGTCACCAATCCACAC 330
Qy 412 GACCTTGACCTTTCTCGAGTACAGCTTTACGCAAGGAGAGTGTCCCGATCTCTCG 471
Db 331 CTCTTGTCCTTCTTGGAGAGGATTTACTACGAGTCCCAGATTT---CGATTTCTCC 387
Qy 472 GGTCTAGCCAGTCCAAAGAACGTTTCGAACCCCACTTACCGTTTCGGTTCCTTAAAGGAAACG 531
Db 388 AGTTTGCCTTCTCCAGACTGATGAACAGCACATATCGCATCTTTCGCTCCCGAGTCT 447
Qy 532 ATCGAGAAACCCGGTGTGAAGTCTGTGCTGTCGCGAACCCGTTTGAACACATTCATC 591
Db 448 GTTAAGAGCTCTCTTGTGAAGATTGTATTGTTGTAGAAACCCCTAAGGACATGTTTGTG 507
Qy 592 TCTTCTGTGCATTTACCAACAACATCAAAATCCGAGTCACTGAGCCAGTCTTGTGTAGAC 651
Db 508 TCTTATGAGCATTTTGGGAAAGAGTAGCTCTCTGAGGAAACCGCGGATATCTTATCGAA 567
Qy 652 CAAGCTTTTGTATTTGTCGCGGAGTGAATGCGGTTTGGGCTTGGCCCTTTTGGGAAACATG 711
Db 568 AAAAGCGTTGAAGCGTTTGTGAAGGGAAGTTTATAGGTGGACCCCTTTGGGATCATATA 627
Qy 712 TTTGGATCTCGGAGAGAGCTTTGAAGAGACCAAGAGAGTCTTCTTTTAAAGGTACGAG 771
Db 628 TTGGAGTACTGTTATGCAAGCCGCGAGAAATCCGAACAGGTTTGTGTTTACTTACTACGAG 687
Qy 772 GATCTCAAGAGACATCGAGACCACTTGAAGAGGCTTGAACCTTTTGAAGGTTCTT 831
Db 688 GAGCTAAAGAGACAGACCCGAGTGTGAGATGAAGCGGATCGCGAGTCTTCTTGAATGTGC 747
Qy 832 TTCACCGAAGAGAGAGAACGAAGGGAGTGTGAAGGCTATCGCCGAGCTGTGTAGCTTC 891
Db 748 TTTATTGAAGAGAGAA---GTGAGAGAGATTGTGAAGTTGTGTAGCTTT 795

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Qy	892	GAGAACTCTGAAGAAGTTGGAGGTGAACAAGTCAAAACCAAGTCGATCGATCAAGAAGCTTTGAGAAT	951
Db	796	GAGAGTTTAACTAATTTGGAAGTTAAACAAGAAGGAAATTCGCAATTTGGAATGAGAGACT	855
Qy	952	CGATTCCTTGTTCGAAAGGAGAAGTGAAGTCGATTGGGTAACTATTGTCACTTCACCTTCAAA	1011
Db	856	AAAACTTCTTTAGAAAAAGGAGAGATTGGAGGATGGAGAGATACTTTGAAGTGAAGTCATTG	915
Qy	1012	GTGAAAGAATTGTGAGCCCTTAGTCGATGACAAAGTTAGGTAGATCTGGTCTCACTTT	1067
Db	916	GCAGAGGAAATTTGATAGAACCATTTGAAGAGAAGTTTAAAGGCTCTGGTCTTTAAATTT	971

RESULT 3

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US-09-938-842A-2049
; Sequence 2049, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAVE, AND METHODS OF USE
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2049
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2049

```

Query Match	21.3%;	Score 229.2;	DB 11;	Length 981;
Best Local Similarity	54.9%;	Pred. No. 2.3e-65;		
Matches 525; Conservative	0;	Mismatches 413;	Indels 18;	Gaps 3;

112	QY	GAAGATGAAGGGCTAAGCTGCGAGTTCCAGAGATGTTGGATTCTTTCTCAAGGAGAGA	171
34	Db	GGGATCAAGATCTGACACAGAAGAAACAGAGCTCTGATCTCTTCTCTTCAAGAGAAA	93
172	QY	GGATGGAGAACTCGTTACCTTTACCTATTCAGGGTTTTGGTGCCAAAGAGATT	231
94	Db	GGTTGGTTATGTAGTGAAATATGAATTCAGGACTTTGGCACACAAAGCTATTTTTA	153
232	QY	CAAGCCATCATGTCTTTCCAAAAACATTTCCAAATCCCTCGAAAAACGAGCTGTTTCTGCC	291
154	Db	CAAGGAATCTTGATCTGCCAAAAACGGTTTGAAGCTAAAGATTCGGACATTATCTCTGTC	213
292	QY	ACCATACTAAATCCGGTACAAACCTGGTAAAGCTTTAACTTTACACATCTCTTAACCGT	351
214	Db	ACTAATCCTAAATCAGGTACCACTTGGTTAAAGCTCTTGCTTTGCTCTCTCTTAACCGA	273
352	QY	CACCGGTTTGATCCGGTTGCTCGCTCGAGTACCAACACAGCTCTTTTTCATCTCCAAACCTCAT	411
274	Db	CACAAGTT--TCCAGTTTCTTCTTCTGGTAAACCATCTCTTCTGGTCAACCAATCCACAC	330
412	QY	GACCTTGTAAGTTCTTCTTCGAGTACAAGCTTTAAGCCAAAGGAGATGTTCCGATCTCTCG	471
331	Db	CTTCTTTGTGCCCTCTTTGGAGGAGTTTACTACGAGTCCACAGATT--CGATTTTCTCC	387
472	QY	GGTCTACGAGTCCAAGAGCTTCGCAACCCACTTACGGTTCCGTTCCCTTAAGGAAACG	531
388	Db	AGTTTGCTCTCTCCAAGACTGATGAACACGCACATATCGCATCTTTCGCTCCCGAGTCT	447
532	QY	ATCGAGAAACCCGGTGTGAAGGTCGTACTTGTGCGGGAACCGGTTTGGACATTCATTC	591

RESULT 4

```

RES001 4
US-10-424-599-82242
; Sequence 82242, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 82242
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_45281C.1
US-10-424-599-82242

```

	Query Match	20.6%	Score 221.8;	DB 13;	Length 787;
	Best Local Similarity 58.2%;	Pred. No. 5.9e-63;			
	Matches 435; Conservative 0;	Mismatches 297;	Indels 15;	Gaps 2;	
Qy	104	AAGCCGAAGAAGATGAAGGCTAAGTGCAGATTCCAAGAGATGTTGGATTCTCTTCTTA	163		
Db	50	AAGCAAGTGAAGAAACAAATTAAGCCAAATTGAAGAGTTAAATCTATCTCTTCTTA	109		
Qy	164	AGAGAGAGATGGAGAACTCGTTACTTTACTATTCCAAGGGTTTTGGTGCCAAGCCA	223		
Db	110	GAGAGAAGGGTTGGATAACACCTATCTCTATTATTCCAAGGCTTTTGGTACTCATCA	169		
Qy	224	AAGAGATTCAAGGCATCATGTCCTTTCCAAAAACATTTCCAATCCTCGAAAAAGACGTCG	283		

Db 170 CTGAATCCAGCCATAAACAACCTTTTCAAAACCAATTCACAGCTAAGGACAAATGATGTTG 229
Qy 284 TTCTGGCCACCATACCTAAATCCGGTACACCTGGCTGAAAGCTTTAAAGCTTTTACCTTTACCAATCC 343
Db 230 TTAATGCTAGTGTTCCTAAATCCGGCCACCACTTGGTTGAAAGCCCTTTACCTTTGCTATTC 289
Qy 344 TTAACCGTCACCGGTTTGATCCGGTTCCTCGAGTACCAACCAACCCCTTTTACCTTTCCA 403
Db 290 TCCATCGCCAGTATTTCTCTCTAG-----AGAACCAACCTTACTTATTTTCA 340
Qy 404 ACCCTCATGACCTTGTACCTTTCTCGAGTACAAAGCTTTAG-----CAAACGGAGATG 457
Db 341 ATCCCATGAACCTTGTGCTCCATTTGAATTTGTCAATTTATGATGAATTAATGGCCAAA 400
Qy 458 TTCCGGATCTCTGGGTCACCAAGTCCCAAGAGCTTCGCAACCCACTTACCGTTCCGGTT 517
Db 401 CTCATGACCTATCCAAATGCCAGGCCAAGAAATTTTGGGACTCATGTTCCCATCTCACTT 460
Qy 518 CCCTAAAGGAACCATCGAGAAACCCGGTGTGAAGGTCGTACTTGTGCGCGAACCCTG 577
Db 461 CATTCGCCCAATCAATTAAGAGACTGACTGTAGATCAATTTATTTGTAGGAATCTAT 520
Qy 578 TTGACACATTCATCTTTCGTGGCATTAACCAACACATCAAAATCCGAGTCAGTGAGCC 637
Db 521 TTGACACCTTTGTTTCTACTTGGGTTTTTGTCAACAAATTTATGCCAAAGTTTTTGCTA 580
Qy 638 CAGTCTCTAGACCAAGCTTTTGATCTGTATTCGGGGAGTGCATCGGGTTTGGCCCGT 697
Db 581 CATTAACCTCTAGAGAACTTTTGAAGATCTGTGAAGGATTAATTTGGCTTTGGTCCAT 640
Qy 698 TTGGGAACATGTTGGATCTGAGAGAGCTTGAAGAGACCCAGAGAAAGTCTTCT 757
Db 641 CTTGGAACCATATAGATTAATTTGGAAGAGAGCAATTTGTCAGCCGGAAGAAAGTTTTGT 700
Qy 758 TTTAAGTACGAGATCTCAAGACGATCGAGACCACTTGAAGAGGCTTCAACTT 817
Db 701 TCTTGAAGTACGAGACCTTAAAGAAATGTTCATTTTATGTGAAGAAATAGCTGAGT 760
Qy 818 TCTTGAAGCTTCCCTTACCGGAAG 844
Db 761 TCTTGGTTGCTTCTCACTAAAGAG 787

RESULT 5

US-09-938-842A-1027
; Sequence 1027, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1027
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1027

Query Match

Best Local Similarity 20.4%; Score 219.2; DB 9; Length 996;
Matches 520; Conservative 0; Mismatches 453; Indels 9; Gaps 2;

RESULT 6

US-09-938-842A-1027
; Sequence 1027, Application US/09938842A

Qy 86 AAATCGCGAGCTCCGAAAGCCGAAGAGATGAAGGGCTAAGCTGCGAGTTCACAGAGA 145
Db 17 AAGCTCATCACTTCCAAACTACATGAAGAGAGCAACAGTTAGTCAAGAAACCAAGAACT 76
Qy 146 TGTGGATCTCTCTTAAGGAGAGAGATGGAGAACTCGTTACCTTTACCTTATTCAG 205
Db 77 TCACTCACTCTCTCACTTCAAGCAAGATTTCAATGGGTTATGGTCTCTACAACTACAAG 136
Qy 206 GCTTTTGGTCCAAAGAGATTCAGGCATCATCTTCCCAAAACATTTCCAAAT 265
Db 137 GTTGTGGTACTATCCAAACACACTCCAAAGCGCTTCTGACGTCGCAAAACATTCAGC 196
Qy 266 CCCTCGAAACCAACGCTGTTCTCGCCACCATACCTTAAATCCGGTACAACTGGGTAAAG 325
Db 197 CACGAGATCTGATATAATCTCTCGCTTCTTGGCCAAAGGTGGAACCACTTGGCTCAAT 256
Qy 326 CTTTAACTTTCAACCTCTTAACCTGACCGTCAACCGTTGATCCGGTTCCTCGAGTACCAAC 385
Db 257 CCTTAATTTCTGCTGTGTACATAGAGAAAGT-----ACGCGGAACCCCTTCAACAC 310
Qy 386 ACCCTCTTTTCACTTCCAAACCTCATGACCTTGTATCTTCTTCGAGTACAAAGCTTTACG 445
Db 311 ATCTTTGCTCTTACAAACCTCATGACCTTGTCCCATTTCTTGAGGTGAGTTATACG 370
Qy 446 CCAACGGAGATGTTCCCGATCTCTCGGGTCTAGCCAGTCCAAAGACGTTCCGAAACCACT 505
Db 371 CTAATAGCCAAATTCGGATCTCGCAAAAGTATCTTCTCTATGATCTTTTCTACACACA 430
Qy 506 TACCGTTCGGTTCCTTAAAGGAACGATCGAGAAACCCGGTGTGAAGTCTGCTACTTGT 565
Db 431 TGCATTTCAACATTCGCTGAAGCCACCAACAAA---GCTTGCAAAACCGTATATGCT 487
Qy 566 GCGGAAACCCGTTTGACACATTCATCTCTTGTGTGATTTACCAACCAACATCAAAATCCG 625
Db 488 GTAGAGGTATCAAGATACGTTGTCTCCGGCTGTCATTAAGAAACATGTTGCTACGCA 547
Qy 626 AGTCAGTACGCCAGTCTTGTAGACCAAGCTTTTGTATCTGATCTGATTCGCGGAGTGATCG 685
Db 548 CCAAGATGGATCAAGCCACTTTTGTAGCTCATGTTTGTGCTTATTTGTAGAGGATCTCT 607
Qy 686 GCTTGGCCCGCTTTTGGGAACACATGTTGGGATCTTGGAGAGAGAGCTTGAAGAGACCAAG 745
Db 608 TATAAGACCTTATTTGGGAACATGATTGAGCTATTGGAAGGGAGCTTGAAGCAAAAG 667
Qy 746 AGAAGTCTTCTTTTAAAGTACGAGGATCTCAAGAGACGACATCGAGACCACTTTGAAGA 805
Db 668 AGAATGTTCTTTTCAATGAGTACGAGAGATTAATTTGAGAGCCTCGTGTTCAGTCAAGA 727
Qy 806 GCTTGCACACTTCTTGTAGAGCTTCTTCCACCGAAGAGAGAAACGAAAGGGAGTTTGA 865
Db 728 GACTCGCCAGTTCTTGTGAATCTCCATCCACCAAGGAAGAGAAAGTGGATCGGTGG 787
Qy 866 AGCTATCCCGAGCTGTGTAGCTTCGAGATCTCAAGAGTTCGAGGTGAGAGTCAAGTCAA 925
Db 788 AGGAGATCTTGAAGTGTGTAGTTTACGAAATTTAAGCAATTTGAGGTTTAAAGAAATG 847
Qy 926 ACAGTGCATCAAGAACTTTGAGAACTCGATCTCTTTCGGAAGAGAGAGAGTGAAGT 985
Db 848 GGACAAACGAGAAATGTTGTGTAGATTTCTCAGGTGTTCTTTAGGAAGAGTGAAGTGTGAT 907
Qy 986 GGTTAACTATTTGTCACTTCCAAAGTGAAGAAATGTCAGCCTTAGTGAAGTCAAGT 1045
Db 908 GGAAGAAATCATCTTACGCCACAAATGCGCAAAACCTTTGATGAGATTTATGACTATAGAC 967
Qy 1046 TAGGTGATCTGGTCTCACTTT 1067
Db 968 TAGGAGACTCCGGTTTGATATT 989

Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US 09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1027
LENGTH: 996
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1027

Query Match 20.4%; Score 219.2; DB 11; Length 996;
Best Local Similarity 53.0%; Pred. No. 5.1e-62;
Matches 520; Conservative 0; Mismatches 453; Indels 9; Gaps 2;
QY 86 AATCTCGCGAGCTCCCGAAGCGAAGAGATGAAGGCTAAGCTGGAGTTCCCAAGAGA 145
DB 17 AAGCTCATCTCTCCCAACTACATGAAGACGACAGCTTAGTCAAGAACCAAGAACT 76
QY 146 TGTGGATCTCTCTTAAGAGAGAGATGGAGAACTCGTTACCTTTACCTATCCAAAG 205
DB 77 TGATCACTCTCTACCTTCAGACAAAGATTTTCATGGGTTATGCTCTCAACATACAAAG 136
QY 206 GGTTTGGTGCCAAAGCAAGAGATTCAGACATCATCTTTCCAAAACATTTCCAAT 265
DB 137 GTTGTGGTACTATCCAAACACATCTCAAGCGGTTCTGAGTCCAAAACATCTCAAGC 196
QY 266 CCCTCGAAAACGAGCTGTTCTGCCACCAPACCTAAATCCGGTACACACCTGGCTAAAG 325
DB 197 CACGAGATACGTATATAATCTCTGCTTTTGGCCAAAGGTGAACACCTTGGCTCAAT 256
QY 326 CTTTAACTTTTCAACATCTTAAACCGTCACCGTTTGTATCGGTTGCTCGAGTACCAAC 385
DB 257 CCTAAATTTTCGCTGTGTATACATAGAGAAAGT-----ACCGCGGAACCCCTCAACAC 310
QY 386 ACCCTCTTTTCACTTCCAAACCTCATGACCTTGTACCTTTCTTCGAGTACAAAGCTTTACG 445
DB 311 ATCCTTTGCTCTTACAAAACCTCATGACCTTGTCCCATTTCTTGAGTTGAGTTATACG 370
QY 446 CCAACGAGATGTTTCCCGATCTCTCGGCTAGCCAGTCCAAAGACGTTCCGAACCCACT 505
DB 371 CTAATAGCCAAATTCGGATCTCGCAAAAGTATTTCTCTATGATCTTTTCTACACACA 430
QY 506 TACGTTTCGGTTCCTTAAAGAAACGATCGAGAACCCGGTGTGAAGTCTGTACTTGT 565
DB 431 TGCATTTACAAGCATTCGGTGAACCCACCAAAA-----GCTTGAACACCGGTATATGT 487
QY 566 GCCGGAACCCGTTTGAACATTCATCTTTGTCGCAATTACCAACCAACATCAATCCG 625
DB 488 GTAGAGGTATCAAGATACGTTTCTCGGCTGCAATTATAGAAACATGTTGCATCGCA 547
QY 626 AGTCAGTACGAGCTCTGTAGAACGATTTTGTATCTGTATTCGCGGGAGTGTACG 685
DB 548 CCAAGATGGATCAAGCACTTTTCAAGTCTATGTTGATGCTTATTTAGAGGAGTCTCT 607
QY 686 GGTTTGGCCGCTTTTGGAAACATGTTGGATCTACTGGAGAGAGAGCTTGAAGAGACCA 745
DB 608 TATATGACCTTATTTGGAAACATGTTTGAAGTCTATTTGAAGGAGGAGCTTGAAGCAAG 667
QY 746 AGAAAGTCTCTTTTAAAGTACGAGGATCTCAAGACGACATCGAGACCAACTTGAAGA 805

DB 668 AGAATGTTCTTTTCATGAAGTACGAGAGATATATTGAGGAGCCCTCGTGTCAAGTCAAGA 727
QY 806 GGCTTGCAACTTTCTTAGAGCTTCCCTTCCCGAAGAGAGGAAACGAAAGGGAGTTGTGA 865
DB 728 GACTCGCGGAGTCTTTTGAATGTCCTTCCCAAGGAAGAAAGAAAGTGGATCGGTGG 787
QY 866 AGCTATCGCCGAGCTGTGTAGCTTCGAGATCTGAAGATTTGGAGGTGAACAAGTCAA 925
DB 788 AGGAGATCTTGAAGTTGTGTAGTTTACGAATTTTAAGCAATTTTGGAGGTTAATAGAATG 847
QY 926 ACAAGTCGATCAAGAACTTTTGAAATCGATTTCTTTTCGAAAGGAGAGTGAAGTGAAT 985
DB 848 GGAACAAGGAAATTTGGTGTAGATTTCTCAGTGTCTTTTAGGAAAGCTGAAGTTGGTGAAT 907
QY 986 GGGTTAACTATTTTCACTTCAACCTTCACAAGTGGAAAGATTTTCAGCTTTAGTGGATGACAAGT 1045
DB 908 GGAAGATCATCTTACGCCACAATTCGCAAAACCTTTGATGAGATTTATGACTATAGAC 967
QY 1046 TAGGTGATCTGCTCTCACTTT 1067
DB 968 TAGGAGACTCCGGTTTGATATT 989
RESULT 7
US-10-437-963-55857
Sequence 55857, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 55857
LENGTH: 1041
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_57824C.1
US-10-437-963-55857
Query Match 18.6%; Score 200.8; DB 17; Length 1041;
Best Local Similarity 56.0%; Pred. No. 7.8e-56;
Matches 448; Conservative 0; Mismatches 337; Indels 15; Gaps 3;
QY 276 CGAGTCGCTTCGCGCACCATACCTAAATCCGGTACACCTGGCTTAAAGCTTTAACTTT 335
DB 225 CGACATCATCTGTCGCACCTTCCCAAGTCCGCGACGAGTGGATCAAGGGCGCTCCTCTA 284
QY 336 CACCATCTTAAACCGTCACTCGGTTTTCGCTCGAGTACCAACCAACCTCTCTTT 395
DB 285 CGCCAGGTGACCG--GAGGAGCACCCCGCCGACCGCCGCGCCGACCCCTTTCA 341
QY 396 CACTTCCAAACCTCATGACCTTGTACTTTCTTCAGTACAAAGCTTTAGCCCAACGAGA 455
DB 342 CTCCTCGGCCCCCAGAGTGGCTCAACTTCTCGAGTACCAGCTCTACCAACAACAG 401
QY 456 TGTTCGCGATCTCTCGGCTAGCAGTCCAAAGACGTTTCGCAACCACTTACCTGCTGG 515
DB 402 AGTCCGGAACCTTGGCAGGCTCCCGAGCCGAGGCTGTTCCGACGACGCTCCGTTTAC 461
QY 516 TTCCTTAAAGGAAACGATCGAGAAACCCCGGTGTGAAGTCTGTGTTACTTTGTCCGGAACCC 575

Db 462 GTGCTGCCGAGCGCGCGCGCGGTGCGGTGCGAGGTGCTGTACGTGTGCGCGCGACCC 521
Qy 576 GTTTGACACATTCATCTCTCGTGGCAATACCAACAACATCAAAATCC---GAGTCAGT 632
Db 522 CAAGGACAACTGATCTCGATGTGGACTTCGCCCAACAAGTTCAAGGCGCGGTGAGGGGCA 581
Qy 633 GAGCCAGCTTGTAGACCAAGCTTTTGATCTGTATTGCGGGGAGTGATCGGTTTG 692
Db 582 GGAGCCCATGTGCGCGGAGGCCATCGCGAGCTGTCTGCTCGCGGTGCGCGGTCCGG 641
Qy 693 CCCGTTTTGGGAACACATGTTGGGACTGAGAGAGAGAGCTTTGAAGAGACCAGAGAAAGT 752
Db 642 GCCGTACTGGACCACTGCTCGGCTACTGGGCGCGCACGTGGCGCGCGCGAGCAGGT 701
Qy 753 CTTCTTTTAAAGTACGAGGATCTCAAGAGACATCGAGACCAACTTTGAAGAGGCTTGC 812
Db 702 CCTCTTCTTCAAGTACGAGGAGATGAAGCTCGACCGCGCGCGCACCGTCCGGAGGCTGGC 761
Qy 813 AACTTTCTTAGAGCTTCTTTCCACCGAAGAGAGAAAGGAGTTGTGAAGGCTAT 872
Db 762 GGAGTTCTGCGCCCTGCGCTTACGCGCGAGAGAGAGAGTGGCGTGTGGACGCCAT 821
Qy 873 CGCCGAGCTGTAGCTTCGAAATCTGAAAGTTGAGGTGAACAAAGTCAAAAGTC 932
Db 822 CGTCAGGCTGTCTCGTTCGATCATGATCGGCTGAGGCGGACCAAGAGCGGCAAGAC 881
Qy 933 -----GATCAGAACTTTGAAATCGATTCTTGTTCGAAAGGAGAGAGTGA 983
Db 882 GGAGCTGTGTGCGCGCGCGGCGGAATAGCTCATCTTCTCGTGGCGGAGTTCGGGA 941
Qy 984 TTGGGTAACTATTGTCACTTCAAGTGGAAAGATTGTACGCTTGTGAGTGA 1043
Db 942 CTGGCGGAACCATCTTTCGCGGAGATTGCACAGCGATCGACCCATTAACCGAGGCGAG 1001
Qy 1044 GTTAGGTGAATGCTGTCTCA 1063
Db 1002 GTTCAATGTTCCGCTCTCA 1021

RESULT 8

US-10-195-144-87/c
; Sequence 87, Application US/10195144
; Publication No. US20030126646A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, GREGORY G.
; APPLICANT: FORMANOVA, NATASHA
; APPLICANT: DENDY, CHARLES
; APPLICANT: LANDRY, BENOIT S.
; APPLICANT: CHEUNG, WING
; APPLICANT: JIN, HUA
; TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 16313-0136
; CURRENT APPLICATION NUMBER: US/10/195,144
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/305,026
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/305,363
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/308,736
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 271990
; TYPE: DNA
; ORGANISM: Raphanus sativum
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (144241)..(144300)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-195-144-87

Query Match 17.1%; Score 184.2; DB 15; Length 271990;
Best Local Similarity 53.5%; Pred. No. 9, 4e-49;
Matches 485; Conservative 0; Mismatches 403; Indels 19; Gaps 4;
Qy 114 AGATGAAGGGCTAAGCTGCGAGTTCCAAGAGATGTTGGATTCTCTTCTTAAGGAGAGG 173
Db 244850 AGACGACAGATAAGTGAAGAAACAGGAAGGTGATCTCTTCTGCTTCTCCACACAGA 244791
Qy 174 ATGCGAAGCTCTTACCTTTTACCTATTCAGAGGGTTTGGTCCCAAGCAAGAGATTCA 233
Db 244790 TTACCAAGGCGCATAGATTGTAATATCAAGGATGTTGGTATATTATACACACCTTCA 244731
Qy 234 AGCCATCATGTCTTTCCAAAAACATTTCCAAATCCCTCGAAAAACAGCTGCTTCTCGCAC 293
Db 244730 AGGTGTC-TCAATTTCCAGAGAGGTTTCAACCGCAAGACACTGATGTAATCATTTGCTT 244672
Qy 294 CATACCTAAATCGGTACAACTGCTGCTAAAGCTTTAACTTTTCAACATCTTAAACGGTCA 353
Db 244671 GTACCCCAATCAGGCACTACTTGGCTCAAGGCCCTCAAGTCTGCTTGTGAGAGATC 244612
Qy 354 CGGTTTGTATCCGGTTCCTCGAGTACCAACCAACCTCTTTTCACTTCCAAACCTTCATGA 413
Db 244611 AAGAACCACTCTTCTG-----ATCATCTCTCTATATATAATCTCTCATGG 244564
Qy 414 CTTGTACTTCTTCTCGAGTACAAGCTTTTACCCCAAGGAGATGTTCCGGATCT---CTC 470
Db 244563 CATTAACCAATCTTGGAGATCGATGTGTACCACCAAGAGCTCAAGTCTCTAAGCTAGCCAA 244504
Qy 471 GGGTCTAGCAGTCCAAAGAACCTTCGCAACCCACTTACCGTTTCGGTTCCTTAAAGAAAC 530
Db 244503 GTTCTCAGCACTTCCAGGCTGTTCTCGACTCAGTCCACAGTCCACAGTCCACAGG 244444
Qy 531 GATCGAAGAACCCGGTGTGAAGTCTGTGATCTTGTGCGCGAACCCTTTTGACACATTCAT 590
Db 244443 ACTCAAGCACTCTCTTGTCAAGATTGTGTACGTGTGCGAAGACGTGAAGGACACGTTGAT 244384
Qy 591 CTCTTCGTGCGATTACACCAACAACATCAAAATCCGAGTCAGTGAGCCAGCTTCTGCTAGA 650
Db 244383 CTGCTGTGGTTTTACAGCTGTGCTATATAATAAATCGAACCACAGAGAGTTCTCGA 244324
Qy 651 CCAAGCTTTTGTATCTGTATTGCGCGGAGTGTATCGGTTTGGCGCTTTTGGGAACACAT 710
Db 244323 GTCTATGTTTAAAGAGTCTCTGATGTGAACCAACTATTTTGGACCTTTTGGGATCATCT 244264
Qy 711 GTTGGATATCTGAGAGAGAGCTTGAAGACACAGAGAAAGTCTTCTTTTAAAGTACGA 770
Db 244263 CTTGAGTTACTGAGAGAGAGCTTGAAGACCCCAAGCATGCTTTTCTTCTGAGGTATGA 244204
Qy 771 GGATCTCAAAGACGACATCGAGACCAACTTGAAGAGGCTTGCACACTTTTCTTAGAGCTTC 830
Db 244203 GGAGATGAAGCGCGAGCTTCGTGATCAGATCAAGAGACTTTCGGGATGCTC 244144
Qy 831 TTTCAACGGAAGAGAGAACGAAAGGAGTTGTGAAGGCTATCGCGGAGCTGTGAGCTT 890
Db 244143 TTTTACTAAGCAAGAGAGATAGTGGATCTGTGCGCGGATCTTGGACCTCTGCTCTCT 244084
Qy 891 CGAGATCTGAAGAACTTCGAGGTGAACAAGTCAACAAGTCAAGATCAAGAACTTTGAGAA 950
Db 244083 GCGTATCTGAGCAGTTTGGAGGCTTAACAA---NACAGGCAACAATAACAATGTGGAGCA 244027
Qy 951 TCGATTCTTTTTCGGAAAGGAGAGTGTGATGGGTTAACTATTGTTACCTTTCACA 1010
Db 244026 CAAATTTTTTTCGTAAGAGAGAGTGTGATGCTGTAACGTAACGTAACGTAACGTAAC 243967
Qy 1011 AGTGGAA 1017
Db 243966 GGAGAAA 243960

RESULT 9

US-10-345-072-87/c
; Sequence 87, Application US/10345072
; Publication No. US20030237112A1


```
/ GENERAL INFORMATION:
/ APPLICANT: BROWN, GREGORY G.
/ APPLICANT: FORMANOVA, NATASA
/ APPLICANT: DENDY, CHARLES
/ APPLICANT: LANDRY, BENOIT S.
/ APPLICANT: CHEUNG, WING
/ APPLICANT: JIN, HUA
/ APPLICANT: LAI, FANG MING
/ APPLICANT: LEFOREST, MARTIN
/ TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN
/ TITLE OF INVENTION: PLANTS
/ FILE REFERENCE: 16313-0210
/ CURRENT APPLICATION NUMBER: US/10/345,072
/ PRIOR FILING DATE: 2003-01-16
/ PRIOR APPLICATION NUMBER: PCT/US02/22217
/ PRIOR FILING DATE: 2002-07-12
/ PRIOR APPLICATION NUMBER: 60/305,026
/ PRIOR FILING DATE: 2001-07-12
/ PRIOR APPLICATION NUMBER: 60/305,363
/ PRIOR FILING DATE: 2001-07-13
/ PRIOR APPLICATION NUMBER: 60/308,736
/ PRIOR FILING DATE: 2001-07-30
/ NUMBER OF SEQ ID NOS: 179
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 87
/ LENGTH: 271990
/ TYPE: DNA
/ ORGANISM: Raphanus sativum
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (144241)..(144300)
/ OTHER INFORMATION: a, t, c, g, other or unknown
US-10-345-072-87

Query Match 17.1%; Score 184.2; DB 16; Length 271990;
Best Local Similarity 53.5%; Pred. No. 9,4e-49;
Matches 485; Conservative 0; Mismatches 403; Indels 19; Gaps 4;

QY 114 AGATGAAGGGCTAAGCTGGAGTCCAGAGATGTGGATCTCTCTCTCAAGGAGAGAGG 173
DB 244850 AGACGACAGATAAGTGAAGAAACAGGAGGTGATCTCTTCGCTTCTTCACACACAGA 244791

QY 174 ATGGAGAACTCGTTACCTTACCTTACCTATCCAGGGTTTGGTCCCAAGCAAGATCA 233
DB 244790 TTACCAAGGCAATAGATTTGTAATATCAAGGATGTGGTATTATTACAAACACCTCCA 244731

QY 234 AGCCATCATGCTTTTCCAAAACATTTCCAAATCCCTCGAAAACGACGTCTCTCGCCAC 293
DB 244730 AGGTGTC-TCAATTTCCAGAGAGGTTTTCACCCGCAAGACACTGATGTAATCATTTGCTC 244672

QY 294 CATACCTAAATCCGCTACAACTGGCTAAAAGCTTTTAATCTTCACTTCACTTCAACCGTCA 353
DB 244671 GTACCCCAATCAGGCACACTCTGGCTCAAGGCCCTCACAGTCGCTCTGCTTGAGATC 244612

QY 354 CCGGTTTCATCCGGTTGCTCGAGTACCAACACCCCTCTTTTCACTTCCAAACCCCTCATGA 413
DB 244611 AAAGAACCACTCTCTG-----ATCATCTCTCTATATCATATCTCTCATGG 244564

QY 414 CTTGTACTCTTTTCAGTACAGCTTTTACGCAACGAGATGTTCCCGATCT---CTC 470
DB 244563 CATTATACCATTTTGGAGATCGATGTGTACCAAGAGCTCAAGTCTCAACCTAGCCAA 244504

QY 471 GGGTCTAGCCAGTCCAAAGAGTTTGGCAACCCACTTACCGTTCCGTTCCCTTAAGGAAC 530
DB 244503 GTTCTCAGACCTCGAGGCTGTTCTCGACTCATAGCCACTGCACAGATCCACGAGC 244444

QY 531 GATCGAGAAACCCGGTGTGAAGTCTGTTGCTGGGAAACCCGTTTGCACATTCAT 590
DB 244443 ACTCAAGCACTCTCTCTTCAAGATTGTGTACGTGTGAGGAACGTGAAGCACAGTTGAT 244384

QY 591 CTCCTCGTGGCATTTACACCAACACATCAATCCGAGTCAGTGAGCCGACCTTCTGTAGA 650
DB 244383 CTCGTGTGGTTTACAGCTGTGTCTATATATAAATCAACCAACCAAGAGTTCTCGA 244324
```

RESULT 10

```
US-10-195-144-80
; Sequence 80, Application US/10195144
; GENERAL INFORMATION:
; APPLICANT: BROWN, GREGORY G.
; APPLICANT: FORMANOVA, NATASA
; APPLICANT: DENDY, CHARLES
; APPLICANT: LANDRY, BENOIT S.
; APPLICANT: CHEUNG, WING
; APPLICANT: JIN, HUA
; TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 16313-0136
; CURRENT APPLICATION NUMBER: US/10/195,144
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/305,026
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/305,363
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/308,736
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 2067
; TYPE: DNA
; ORGANISM: Raphanus sativum
US-10-195-144-80
```

```
Query Match 15.4%; Score 166; DB 15; Length 2067;
Best Local Similarity 53.7%; Pred. No. 5.6e-44;
Matches 421; Conservative 0; Mismatches 345; Indels 18; Gaps 3;

QY 237 CATCATGTCTTTCCAAAAATTTCCAAATCCCTCGAAAACGACGCTGTTCTCGCCACCAT 296
DB 282 CATTTCCTCGGTTTGGAGAGTTTTCACCGCAAGACACTGATGTAATCATTTGCTTCGTA 341

QY 297 ACCTAATCCGTTACAACTGCTTAAAGCTTTAACTTTCACATCTTAAACGTCACCG 356
DB 342 CCCCAATCAGGCACTACTTGGCTCAAGGCCCTCAGTCGCTCTGCTTTGAGAGATCAA 401

QY 357 GTTTGATCCGGTTGCTCGAGTACCAACCAACCTCTTTTCACTTCCAAACCTCATGACT 416
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Db 402 GAACACATC-----TTCTGATCATCTCTCTATATCATATCTCATGCGAT 449
Qy 417 TGTACCTTTCTTCGAGTCAAGCTTTAGCCAAAGGAGATGTTCCCGATCT---CTCGGG 473
Db 450 TATACCAATCTTGGAGATCGATGTGTACACGAAAGCTCAAGTCTTAACCTAGCCAAAT 509
Qy 474 TCTAGCCAGTCCAGAAAGCTTGGCAACCACTTACCGTTGCGTTCCCTAAAGGAAAGCAT 533
Db 510 CTCAGCACTCCGAGCTGTTCTGATCATATGATCCCACTGACAGATCCAGAGCACT 569
Qy 534 CGAGAAACCCGGTGTGAAGGTCTGTACTTGTGCGGAAACCGTTTGACACATTCATCTC 593
Db 570 CAAAGCACTCTCTTGCAGAAATGTGTACGTGTGAGGAAAGCTGAAGGACACGTTGATCTC 629
Qy 594 TTCGTGGCATTTACACCAACCACTCAATCCGAGTCACTGAGCCAGCTTCTGCTAGACCA 653
Db 630 GTGTTGGTTTACAGCTGTGCTATATATAAAATCGAACCAACCAAGAGATTTCTGAGTC 689
Qy 654 AGCTTTTGATCTGTATTTGCGGGGAGTGTATCGGGTTTGGCCCGTTTGGGAACACATGTT 713
Db 690 TAGTGTTAACGAGTCTCGGATGGAACCACTATTTTGGACCTTTTGGGATCATCTCT 749
Qy 714 GGGATCTGGAGAGAGCTTGAAGAGGAGTGTGAAGGCTATGCGCGAGCTGTGTAGCTTGA 773
Db 750 GAGTTACTGGAGGAAAGCTTGAAGAGCCAAAGCATGTCCTTTTCATGAGGTATGAGGA 809
Qy 774 TCTAAGAGCATCGAGACCAACTTGAAGAGGCTTGCACCTTTCTTAGAGCTTCTTTT 833
Db 810 GATGAAGCCGAGCTCTGATCATCATGAGACTTGGGACCTTCTGACCTCTCTCTGCG 869
Qy 834 CACCGAAGAGGAGGAGGAGGAGTGTGAAGGCTATGCGCGAGCTGTGTAGCTTGA 893
Db 870 TACTAAGCAAGAGAGATAGTGGATCTGTGACCGGATCTTGGACCTCTCTCTGCG 929
Qy 894 GAATCTGAAGAGTGGAGGTGAACAGTCAACCAAGTCAAGAGCTTGAAGAGTGTGAAGTCG 953
Db 930 TAATCTGAGCACTTTGGAGGCTAAACAA---AACAGGACAAATAAACAATGTGGAGCA 986
Qy 954 ATTCTTTTTCGAAAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1013
Db 987 GTTTTTCGTAAGGAGAGTGGTGACTCGGAAATATCTTACGTTCTGAAATGGA 1046
Qy 1014 GGAA 1017
Db 1047 GAAA 1050

RESULT 11
US-10-345-072-80
; Sequence 80, Application US/10345072
; Publication No. US20030237112A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, GREGORY G.
; APPLICANT: FORMANOVA, NATASA
; APPLICANT: DENDY, CHARLES
; APPLICANT: LANDRY, BENOIT S.
; APPLICANT: CHEUNG, WING
; APPLICANT: JIN, HUA
; APPLICANT: LAI, FANG MING
; APPLICANT: LEFOREST, MARTIN
; TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN
; FILE OF INVENTION: PLANTS
; FILE REFERENCE: 16313-0210
; CURRENT APPLICATION NUMBER: US/10/345,072
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/22217
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/305,026
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/305,363
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/308,736

; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 2067
; TYPE: DNA
; ORGANISM: Raphanus sativum
US-10-345-072-80

Query Match 15.4%; Score 166; DB 16; Length 2067;
Best Local Similarity 53.7%; Pred. No. 5.6e-44;
Matches 421; Conservative 0; Mismatches 345; Indels 18; Gaps 3;

Qy 237 CATCATGTCTTTCCAAAACATTTCCATCCCTCGAAAACGACGTCTCTCCGCCACCAT 296
Db 282 CATTTTCCGGTTTGGAGAGTTTTCACCCGAAGACACTGATGATTAATCATTTGCTTCGTA 341
Qy 297 ACCTAATCCGTTACAACTGCTTAAAGCTTTAACTTTCAACCATCTTTAAACCGTCACCG 356
Db 342 CCCCAATCAGGCACTACTTGGCTCAGGCCCTCAGTCGCTCTGCTTGAGAGATCAAA 401
Qy 357 GTTTGATCCGGTTGCTCGAGTACCAACCACTCTTTTCACTTCCAAACCTCATGACCT 416
Db 402 GAACCACTC-----TTCTGATCATCTCTCTATATATAAATCTCTCATGTCAT 449
Qy 417 TGTACCTTTCTTCGAGTCAAGCTTTTACGCCAAGGAGATGTTCCCGATCT---CTCGGG 473
Db 450 TATACCAATTTTGGAGATCGATGTGTACCAAGAGCTCAAGTCTTAACCTAGCCAAAT 509
Qy 474 TCTAGCCAGTCCAAAGAACTTTCGCAACCCCACTTACCGTTTCGGTTCCCTAAGAGAAACGAT 533
Db 510 CTGAGCACTCCGAGCTGTCTCGACTCAGATGCCATGACACGATCCAGAGCACT 569
Qy 534 CGAAGAACCCGGTGTGAAGTGTGTACTGTGTGCGGAAACCGTTTGACACATTCATCTC 593
Db 570 CAAGCACTCTCTCTGCAAGATTTGTACGTGTGAGGAAAGCTGAAGGACACGTTGATCTC 629
Qy 594 TTCGTGGCATTCACCAACCAACATCAATCCGAGTCACTGAGCCCACTTCTCTAGACCA 653
Db 630 GTGTTGGTTTACAGCTGTGCTATATAAATCGAACCAACCAAGAGAGTTCGAGTC 689
Qy 654 AGCTTTTGATCTGTATTTGCGGGGAGTGTATCGGGTTTGGCCCGTTTGGGAAACATGTT 713
Db 690 TATGTTTAAAGGCTTCTGCGATGGAACCAACTATTTTGGACCTTTTGGGATCATCTCT 749
Qy 714 GGGATCTCGAGAGAGCTTGAAGAGACACAGAAAGTCTTCTTTTAAAGGTACGAGGA 773
Db 750 GAGTTACTGGAGAGAGCTTGGAAAGCCCAAGCATGTCTCTTTTTCATGAGGTATGAGGA 809
Qy 774 TCTCAAAGACGATCGAGACCAACTTGAAGAGGCTTGAACCTTTCTTGAAGCTTCTCTTT 833
Db 810 GATGAAGCCGAGCTCTGATCATCATGAGACTTGGGAGCTTCTTGGGATGTCCTTT 869
Qy 834 CACCGAAGAGAGGAGGAGGAGTGTGAAGGCTATGCGCGAGCTGTGTAGCTTGA 893
Db 870 TACTAAGCAAGAGAGATAGTGGATCTGTGACCGGATCTTGGACCTCTCTCTGCG 929
Qy 894 GAATCTGAAGAGTGGAGGTGAACAGTCAACCAAGTCAAGAGCTTGAAGAGTGTGAAGTCG 953
Db 930 TAATCTGAGCACTTTGGAGGCTAAACAA---AACAGGACAAATAAACAATGTGGAGCA 986
Qy 954 ATTCTTTTTCGAAAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1013
Db 987 GTTTTTCGTAAGGAGAGTGGTGACTCGGAAATATCTTACGTTCTGAAATGGA 1046
Qy 1014 GGAA 1017
Db 1047 GAAA 1050

RESULT 12
US-10-437-963-55524
; Sequence 55524, Application US/10437963

Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 5524
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_57523C.1
US-10-437-963-5524

Query Match 15.0%; Score 161.8; DB 17; Length 1077;
Best Local Similarity 51.1%; Pred. No. 9.5e-43;
Matches 444; Conservative 0; Mismatches 407; Indels 18; Gaps 2;

QY 205 GGGTTTGGTCCAGCAAGAGATTCAAGCCATCATGTCTTCCAAAACATTTCCAA 264
Db 175 GGATTCTGTACCGCGGCACCTGATCGCGCGACGTGGCGCGGAGACATGTCGTG 234
QY 265 TCCCTCGAAAAACGACGTCTCTGCCACCATCTAAATCCGGTACAACTGGCTAAAA 324
Db 235 GCCCGCCCCAGCGATCATCTCGCACCATGCCAAGTCCGACTCGAGTGGCTCAAG 294
QY 325 GCTTTAACTTTACATCTTAAACGTCACCGGTTTGAATCGGTTGCTCGAGTACCAAC 384
Db 295 CGCGTCGCTTCTGCTGTCAGCGCGGCGCCACGCGCGCGCGCGCGCGCGCGCGCG 354
QY 385 CACCTCTTTTCACTTCCAACTTCACTGACCTTCTTCTTCTGAGTACAGCTTTAC 444
Db 355 CTCTCTCACTCCAGCGCGACGCTGTCGTCATCTCTGACTCCATCTACGAGATCAGC 414
QY 445 GCCAACGGAGATG-----TCCGATCTCTCGGCTTAGCAGTCCAAAGAACGTTTC 495
Db 415 CGCAGTCCGCGTCCGCCAGGCCATCGCTCGATGCGTCCGCGCGCATCTG 474
QY 496 GCACCCCACTTACCGTTCCGTTCCCTAAGAAACGATCGAAACCCGCGTGTGAAGTC 555
Db 475 GCAGTGCACGAACCGCTCTCGAGCGTCCCGCGTCCGCTCAAGCGCTCCGCGTCCGCG 534
QY 556 GTGTACTGTCCGGAAACCGGTTTGACACATTCATCTCTTCTGTCGCAATTACCAACAA 615
Db 535 GTCTACCTGTCCCGGACCCCAAGACGCTTCTGCTCGCTCCGCGATTAATCTCGACG 594
QY 616 ATCAAAATCCGAGTCAGTGAGCCAGTCTTGCTAGACCAAGCTTTTGTATCTGTATTC 675
Db 595 ATCAAAACAGAGGATCCACCATGACGCGGTTCCGACGAGGCTTCGAGCTGCTCGGAC 654
QY 676 GGAGTGTGCGGTTTGGCCCGTTTGGGAACACATGTTGGATCTCGAGAGAGAGCTTG 735
Db 655 GCGGTCTCGCGTACGGGCGCTTATGTTGGGACACCGCGCGCGAGTACTGGAAGGAGG 714
QY 736 AAGAGACAGAGAAAGTCTCTTTTAAAGTACGAGGATCTCAAAGACGACATCGAGACC 795
Db 715 GCGCGCGCGAGGAGGTGCTGCTCTCTCGGTACGAGAGCTTCAAGGAGGACGCGGTGG 774
QY 796 AACTTGAAGAGCTTGCACTTTCTTAGAGCTTCTTTTCCCGAAGAGAGAGAAAG 855
Db 775 AGCGTGAAGGCGCTCGCGCGCTTCTCGGCTGCGCGCTTCAACCGCGAGAGCTTGC 834
QY 856 GGAGTTGTGAAGGCTATCGCGCGAGCTGTGTAGCTTCGAGATCTGAAGAAAGTTGAG 915

Db 835 GCGTCCCCGAAACTATCTGTGAGCTCTCGAGTATGAAAGGATGAGAAACGTGGAGCA 894
QY 916 AA-----CAAAGTCAAAACAAAGTCGATCAAGAACTTTGAGAATCGATTTCTGTT 966
Db 895 AATCGAGACGGGAGCACGCGGCTACTGTCGTCTCAAGAACTTCGCGCTTCTTCAGG 954
QY 967 AAGGAGAAAGTGAAGTGAATTTGGTTAACTATTTGTACCTTCAAGTGAAGAAATGTCA 1026
Db 955 AAGGGTGAAGTGGAGACTGGAAGGAGCACATGTGCGCGAGATGCGCGGAGGCTCGAC 1014
QY 1027 GCCTTAGTGAATCACAAAGTTAGTGGATC 1055
Db 1015 GACGTCGTGAGGAGAAAGCTGCGAGGCTC 1043

RESULT 13
US-10-021-323-11330
; Sequence 11330, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd B.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 11330
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(654)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3829-001-Q1-K6-G6
US-10-021-323-11330

Query Match 14.6%; Score 157; DB 17; Length 654;
Best Local Similarity 56.9%; Pred. No. 2.8e-41;
Matches 355; Conservative 0; Mismatches 251; Indels 18; Gaps 3;

QY 294 CATACCTAAATCCGCTAACCTGGCTAAAGCTTTAACTTTCACCATCTTAAACGCTCA 353
Db 1 CTTTTCAAAATGTGGTACTACTTGGCTCAAGGCTTGACTTTCTCCACTTTGTACCGCAA 60
QY 354 CGGTTTGTATCCGTTGCTCGAGTACCAACCACTCTTTTCACTTCCAAACCTCATGA 413
Db 61 TCAGTTCCCATGGATG-----AAATTCATGCTCACTTTGGCGCTTCACTCA 108
QY 414 CTTGTACCTTTCTTTCGAGTACAAGCTTTACGCCAAACGAGATGTTCCGATCTCTCGG 473
Db 109 ACTTGTGCTTCTTTCGAGTATGATCTTACTTTGAACAACCCCTTTTCTCTGATCTT 168
QY 474 TCTAGCCAGT-----CCAGAACGTCGCAACCCACTTACCGTTCCGTTCCCTAAG 528
Db 169 GTTGTGCTTATCAGCAAGGCTTTTTCACCCAGGCTTTATGCTACTTTGCAACT 228
QY 529 AGCATCGAGAAACCCGGTGTGAAGTGTGATGTTGTCGCGGAAACCCGTTTGACACATTC 588
Db 229 TCCATTAAAGATTCGCGTGTAAAGTTGTTACATATGTAGAAACCCCATGATATCTTC 288
QY 589 ATCTCTTCGCTGAGATTAACCAACAACTCAAAATCGAGTCAAGTCCAGCCAGCTTGT 648
Db 289 ATTCTCTTTTGGCTTTCTCTGCAAGCTCCGAGACAAAAACCAAGAGTCACTATCACTA 348
QY 649 GACCAAGCTTTTGTATCTGTATTGCGGGGAGTGTGCGGCTTTTGGCCGCTTTTGG 708

Db 349 GATGAAGCTTTTGACAAAGTTCTACCAATCTCTGCGATGACCAATTTTGTATCAT 408
 QY 709 ATGTTGGATACCTGGAGAGAGCTTGAAGACACAGAAAGTCTTCTTTTAAAGTAC 768
 Db 409 GTATTGGATATTGAAGGCAAGCAAGAAACCCCAACAAATATTGTTTGAATTT 468
 QY 769 GAGGATCTCAAGAGCAGCATCGAGACCAACTTGAAGAGGCTTGAACATTTCTTAGAGCTT 828
 Db 469 GAAGATCTTAAGGAAGATATGATTCATTTGAAATTTTGGCCATGTTCTTAGGAGTT 528
 QY 829 CCTTTCACGGAAGAGGAACGAAAGGAGTTGTGAAGGCTATCGCGAGCTGTGAGC 888
 Db 529 CCTTTCACAGATGATGAAGAAACAGGNAGTTGTTGA-AAAATAGCAAAATTTGAGC 587
 QY 889 TTCGAGATCTGAAGAAGTTGGAG 912
 Db 588 TTGAGAACTTGAAGAATTGAAG 611

RESULT 14

US-10-437-963-94656
 ; Sequence 94656, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 94656
 ; LENGTH: 1068
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_92925C.1
 US-10-437-963-94656

Query Match 14.4%; Score 155; DB 17; Length 1068;
 Best Local Similarity 53.1%; Pred. No. 1.8e-40;
 Matches 438; Conservative 0; Mismatches 360; Indels 27; Gaps 4;
 QY 277 GACGTGCTTCGCGACCATACCTAAATCCGGTACACCTGGCTAAAGCTTTAACTTC 336
 Db 238 GACATCGTGGTCCCGACCCCTGCCAAGTCCCGGACGAGTGGATCAAGGCGCTCTCTAC 297
 QY 337 ACCATCTTAAACCGTCAACGGTTTATCGGTTGCTCGAGTACCAACCCCTCTTTTC 396
 Db 298 GCCACGGTGACCG--GAGAGAGCATCCCGCGAGCGCGCGGACCAACCCCTTCAAC 354
 QY 397 ACTTCAACCTCATGACCTGTGATCTTCTTCGAGTACAGCTTTAGCCCAAGGAGAT 456
 Db 355 TCCCTCGCGCCCGCCAGAAATGGTCAAAATCTCTCGAGTACCATCTCTACAGGCGGAG 414
 QY 457 GTTCCCGATCTCTCGGCTAGCCAGTCCCAAGAGGTTTCGCAACCCCACTTACCGTTCCGT 516
 Db 415 GCCCGCGACCTCGAGCGCTCCCGGACCGCGGTGTTGCGAGCAGCGCGCGTTCGAC 474
 QY 517 TCCCTAAAGAAACGATCG-----AGAAACCGGTGTGAAGTGTGTACTTG 564
 Db 475 CTCCTCGCGGAGCGGTGTCGCGCGCGCGCGGTTCGGGCTGCAAGGTGCTTACGTG 534
 QY 565 TSCCGGAACCGGTTTGACATTCATCTCTTCGTGGCATTACCAACAAACATCAAAATCC 624

Db 535 TCCCGTACACCCCAAGACACACCTGCTCTCCCTCTCTGCAAGTTCGTCACGAGTACAGTCC 594
 QY 625 GAGTCAGTGTAG---CCCAAGTCTGTAGACCAAGCTTTTGTATCTGTATTTCGGGGAGTG 681
 Db 595 CGGAACGGGAGGAGCTCGTCCAGTGGAGCGCGCGTGGGCTTCTTCTGCGACGGCGTG 654
 QY 682 ATCGGTTTGGCCGCTTTTGGGAACACATGTTGGATACCTGGAGAGAGCTTGAAGAGA 741
 Db 655 TGCCGCTTCGGGCCCTACTGGGAGACGCTCTCGGCTACTGCGCGCCACCGGGAGCGC 714
 QY 742 CCAGAGAAAGTCTCTCTTTTAAAGTACGAGGATCTCAAGACGACATCGAGACCAACTTG 801
 Db 715 CCGAGCGGCTCTCTTCTCAGGTACGAGGAGATGAAGCGGACCCCGCGGGCACGTG 774
 QY 802 AAGAGCTTGCACCTTCTTAGAGCTTCTTTCACCGAAGAGAGAAACGAAAGGAGTT 861
 Db 775 CGGAGGCTGGCGAGTTCGCCGGGCTCCCTTCACTCGCGGAGAAAGACGGCGGCGCG 834
 QY 862 GTGAAGGCTATCGCGAGCTGTAGCTTCGAGAATCTGAAGAGTTCGAGGTGAACAAG 921
 Db 835 GTGGACGCAATGTCAAGCTGTGCTGTTTCAACATGTTGCGGCTGGAGCGGACCAAG 894
 QY 922 -----TCAACAAGTCGATCAAGAACTTTGAGAATCGAATCTTGTTCGGAAGA 972
 Db 895 GGTGGCGCGACGAGCTCAACACCAACACCGTTCGGAACAGCGCGCTTCTTCGGCGTGA 954
 QY 973 GAAGTCAAGTATGGGTTAACTATTGTCACTTCAAGTTCGAAAGATGTCACGCTTA 1032
 Db 955 GAGGTGGAGACTGGGCGAACCATCTGCTTCGGAGATGGGCGCAACGAATGACGCCATC 1014
 QY 1033 GTGGATGACAAAGTATAGTGGATCTGCTCTCACTTTTCAGGTTGAGC 1077
 Db 1015 ACCGAGCTAAGTTTGCAGTTTTCGCTAGCGCCAGCCCTGATC 1059

RESULT 15

US-10-259-165-331
 ; Sequence 331, Application US/10259165
 ; Publication No. US20030135888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Chang, Hur-song
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiyuki
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Moughamer, Todd
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Rickes, Darrell
 ; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
 ; FILE REFERENCE: 70030-NP
 ; CURRENT APPLICATION NUMBER: US/10/259,165
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; PRIOR APPLICATION NUMBER: US 60/368,327
 ; PRIOR FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; NUMBER OF SEQ ID NOS: 782
 ; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
 ; SEQ ID NO 331
 ; LENGTH: 1041
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 US-10-259-165-331

Query Match 13.7%; Score 147.4; DB 15; Length 1041;
 Best Local Similarity 53.9%; Pred. No. 6.2e-38;
 Matches 376; Conservative 0; Mismatches 306; Indels 15; Gaps 3;

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Qy 237 CATCATGTCCTTTTCAAAAACATTTCCRAATCCCTCGAAAAAGAGTCGTCTTCGGCCACCAT 296
Db |||||
Qy 177 CGTCATGGTGGCGAGCGCCACTTTCACCGCCCGGACACCGACATCATTCGCCACCTT 236
Db |||||
Qy 297 ACCTAATCCGGTACAACTCGCTAAAGCTTTAACTTTACCAATCCTTAACCGTCACCG 356
Db |||||
Qy 237 CCCCAGGTGTGGACCACTCGCTCAAGCGCTCCTCTTCGCGACCGTCCACCGCGACGG 296
Qy 357 -GTTTGATCCGGTTGCTTCGAGTACCAACACCTCTTTTCACTTC-----AACCC 407
Db |||||
Qy 297 CGGGCGCCCGCGGCTTGGAGGACGAGCGCGCGCTCGGCAGCTCAGGGCGGGAACCC 356
Qy 408 TCATGACCTTTACCTTTCTTCGAGTACAAGCTTTAGCCAAACGAGATGTTCCCGATCT 467
Db |||||
Qy 357 GCACGAGCTCTCCGCTTCTTCGAGATCCAGGTGTACGTGCGGACAGGGCGGCCGACCT 416
Qy 468 CTCGGGCTACCGAGTCCAGAACGTTCCGAACCCACTTACCCTTCGTTCCCTAAAGGA 527
Db |||||
Qy 417 GAGTCCTCTCCCGCGCCACCGGCTCTCGGACGACATCCCGCGCCCTCCCTGCCGCG 476
Qy 528 AACGATCGAGAAACCGGCTGTGAAGTCTGTACTGTGCGGAAACCGCTTGCACACTT 587
Db |||||
Qy 477 CTCGTCGCCATCTCCGCTCAAGGTGGTGTACATGTGCGCGACCCCAAGGACTGCCT 536
Qy 588 CATCTCTTCGTGGCAATTACACCAACAACATCAAAATCCGAGTCAGTGAGCCCAAGTCTTGCT 647
Db |||||
Qy 537 CGTCTCGCTGTGGCACTTCTTGAGCGCGCAGCGCGCGAGCCACGCGCGACGCTC----- 591
Qy 648 AGACCAAGCTTTTGCATCTGTATTCCCGGGAGTGATCGGTTTGGCCGCTTTGGGAACA 707
Db |||||
Qy 592 -GGCGAGACTTCCGCTCTTCTCGACGGCGTCTCGTGGTGGGCCGCTACTGGGACCA 650
Qy 708 CATCTTGGGATCTGGAGAGAGACTTTGAAGAGACCAGAGAAAGTCTTCTTTTAAAGTA 767
Db |||||
Qy 651 CGTCTGGCTTACTGGCGTGGCACGTTCGAGCGCCCGGGCAGGTGCTGTTTCAAGCTA 710
Qy 768 CGAGGATCTCAAGACGACATCGAGACCACTTGAAGAGGCTTGCACACTTCTTAGAGCT 827
Db |||||
Qy 711 CGAGGAGTGAAGCGGACACGCTGGGCGAGCTGCGCCCTCGCGAGTTCGTCGGCCG 770
Qy 828 TCCCTTTCACCGAAGAGAGAAACGAAAGGGAGTTGTGAAGGCTATCGCCGAGCTGTGTAG 887
Db |||||
Qy 771 GCCGTTCAACCGCGAGAGCGGGCGGCCCGGGTGGACGAGGCGATCGTGAAGGGGTGCAG 830
Qy 888 CTTGAGAACTGAAGAGTTGGAGGTGAACAAGTCA 924
Db |||||
Qy 831 CTTGAGAGCTTAGCGGCGCGGAGGTGAACAGGTCA 867
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Search completed: August 17, 2004, 07:12:21
Job time : 1842 secs

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